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JOURNAL Patent: WO 02061087-A 517 08-AUG-2002;  
 Lifespan Biosciences, Inc. (US)

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LOCUS AX029424  
DEFINITION Sequence 4 from Patent WO915551.

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VERSION AX029424.1 GI:10190217  
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ORGANISM Homo sapiens (human)  
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BD062446 2834 bp DNA linear PART 27-AUG-2002  
LOCUS



DEFINITION Novel receptor.  
ACCESSION BD062446  
VERSION BD062446.1 GI:22608049  
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REFERENCE Herzog,H.  
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TITLE Patent: JP 2001513653-A 2 04-SEP-2001;  
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DEFINITION CQ768015  
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VERSION CQ768015.1  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Wood, W. I., Goddard, A., Gurney, A., Yuan, J., Baker, K. P. and Chen, J.  
TITLE Human neurotrophin homologue  
JOURNAL Patent: EP 1386931-A 482 04-FEB-2004;  
Genentech, Inc. (US)  
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ORIGIN  
Query Match 98.6%; Score 2783.4; DB 6; Length 3819;  
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Qy 64 AACCTCAGCTCCCGGGTTCAAGTATTTCTATGCTTCAGCTTCCGAGTACGCTGGATT 123  
Db 115 AACCTCAGCTCCCGGGTTCAAGTATTTCTATGCTTCAGCTTCCGAGTACGCTGGATT 174  
Qy 124 ACAGGTGTGATCTTCCAGAGTGACTCCGTCGAGGAAATGATCCCGAGTCCGCTGAG 183  
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Qy 184 CAGACGACATGTTCTGTGAGTCTGTCTTCTGTGTCAGAGTCCCAAGGAGGAGGAG 243  
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ACCESSION AX358880.1 GI:18675341  
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Baker, K.P., Desnoyers, L., Gerltsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
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VERSION AX454506.1 GI:21713877  
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REFERENCE  
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Goddard, P., J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Disorders involving angiotensin  
Patent: WO 0208284-A 91 31-JUN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 REFERENCE  
 AUTHORS Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Flvaroff, B.,  
 Gao, W.Q., Geriltsen, M.E., Goddard, A., Godowski, P.J., Garney, A.L.,  
 Sherwood, S., Smith, V., Stewart, T.A., Tumbas, D., Watanabe, C.K.,  
 Wood, W.L. and Zhang, Z.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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ACCESSION AX490984  
VERSION AX490984.1 GI:22323829

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

1 Baker, K.P., Ferrara, N., Gerber, H., Gertlzen, M.E., Goddard, A.,  
Godowski, P., Gurney, A.L., Hillen, K.J., Marsters, S.A., Pan, J.,  
Poon, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
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Compositions and methods for the diagnosis and treatment of  
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Patent: WO 0200690-A 91 03-JAN-2002;

Genentech, Inc. (US)

Location/Qualifiers

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DB 475 TACCACTTTCCTGCTTATCTGAAACCGAATGTGTGGAGATTAATCTTCTCTATGGCAAG 534

QY 484 CTGACTTCTTCTGCTGATGACAAAGCTCTTACGCTTCTGCTTCCAGACACAGAGAG 543  
DB 535 CTGACTTCTTCTGCTGATGACAAAGCTCTTACGCTTCTGCTTCCAGACACAGAGAG 594  
QY 544 AGCCTGCTCAGAGGAGCCCGCTGTTAGCACTTCTGTGCACTCTCTGTGAGAGCCCTCAG 603  
DB 595 AGCCTGCTCAGAGGAGCCCGCTGTTAGCACTTCTGTGCACTCTCTGTGAGAGCCCTCAG 654  
QY 604 AACATCAGCTTCGACAGTGCAGCTTCACTTCTCTTCCATCAGTCTTCCCAACAG 663  
DB 655 AACATCAGCTTCGACAGTGCAGCTTCACTTCTCTTCCATCAGTCTTCCCAACAG 714  
QY 664 GCGCTTCACAAATGCTTCGCTGAGCAGTGTGAGCTCAAAAGAGAGCCCTCAGCTCAGC 723  
DB 715 GCGCTTCACAAATGCTTCGCTGAGCAGTGTGAGCTCAAAAGAGAGCCCTCAGCTCAGC 774  
QY 724 CAGTTCCTGAGAGATCCCAAGAGGCTCAAGAGAGCCCTCGAGCTGCCCCCGCAGCAG 783  
DB 775 CAGTTCCTGAGAGATCCCAAGAGGCTCAAGAGAGCCCTCGAGCTGCCCCCGCAGCAG 834  
QY 784 CAGTTCAGAGCTTCAGAGTGAATCTGATCTTGTGAGATTTCAATGGAGAGCATGTGTC 843  
DB 835 CAGTTCAGAGCTTCAGAGTGAATCTGATCTTGTGAGATTTCAATGGAGAGCATGTGTC 894  
QY 844 TTGAGAGAGAGCCGAGATCAAGCCAGGATGAGAGCTCCAGCCACAGCCGCTCAG 903  
DB 895 TTGAGAGAGAGCCGAGATCAAGCCAGGATGAGAGCTCCAGCCACAGCCGCTCAG 954  
QY 904 GACCTGCAATCCACTCCCGGAGAGAGAGAGAGAGAGAGATCATGAGATCTCGGTG 963  
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QY 1024 CTGCTGCTTGAACACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083  
DB 1075 CTGCTGCTTGAACACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1134  
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QY 1324 CTGATGATCTTCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383  
DB 1375 CTGATGATCTTCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1434  
QY 1384 TACGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443  
DB 1435 TACGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494  
QY 1444 TCCAGAGTGCCTTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1503  
DB 1495 TCCAGAGTGCCTTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1554  
QY 1504 AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1563  
DB 1555 AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1614  
QY 1564 CTGAGAGGCTGAGAGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623





Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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QY 4 CAGCAGGCTGCTGCTGTCACACAGGCTGAGTGCAGTGTGATCTTGTCAATCGT 63
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QY 64 AACCTCACTCCCGGTTCAAGTATCTCATGCTCCAGCTCCCGAGTAGCTGGATT 123
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QY 124 ACAGGTGTGATCTTCCAGAGTGAATCCGTCGAGAGAAATGACTCCCACTGCTGCTG 183
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Db 235 CAGACGACATGTTCTGCTGATGATCTGCTTCTGATCCAGAGTCCAGAGGAGC 294
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QY 304 TACAAACCCACACAGAGCTGCGCATCTCATGAGAACTCCAGAGGCTTCACAGTC 363
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QY 484 CGGACCTTCTGCTGATGAGCAAGGCTGAGCTCTGCTGCTTCCAGACACAGAGAG 543
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Db 655 AACATGAGCTGCGCCAGTGCAGGCTTCACTTCTTCCCAAGTCTCCCAACAG 714
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Db 715 GCCGCTCAATGCTGCTGATGAGCATGTGCGAGCTCAAAAGGAGCTTCAGCTGCTAGC 774
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Db 955 GACCTGCAATCCATCTCCCGAGAGAGAGAGAGAGAGAGATCATGAGTACTCGGTG 1014
QY 964 CTGCTGCTGGAACACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1023
Db 1015 CTGCTGCTGGAACACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1074
QY 1024 CTCTCTGTGTGACTTCAAGAGCCAGGCTGTTCAGAGCAAGAAATTCAGCCAGTTC 1083
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QY 1144 CCGGTGTGTCTACTTTCCAGAGCCAGCTACAGCCGAGAGAGAGAGAGAGAGAGAGAG 1203
Db 1195 CCGGTGTGTCTACTTTCCAGAGCCAGCTACAGCCGAGAGAGAGAGAGAGAGAGAGAG 1254
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QY 1384 TACGTGGCTGTGTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
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Db 1915 CTGCTGAGTCAATCAACCAACTGAGCTCTTCAAGCTGTGTGTCTGTCAACATGAGCC 1974
QY 1924 ATGCTAGCAATGATGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1983
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QY 1984 CATGTGCAATCACTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2043
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QY 2044 TTCTCTTGTGCTTGTGAGCACTTCAGCTTGTGTCTGTCTGTCTGTCTGTCTGTCTGT 2103
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Db 2155 TCTTTCAGAGCTTCTCAATCTGATCTGTGATGATGATGATGATGATGATGATGATGAT 2214
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## ORIGIN

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Query Match 98.4%; Score 2778.2; DB 9; Length 3702;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2806; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

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62 CTTCCACCTCCCGGGTTCAAGTATCTCATGCTCAGCTCCCGAGTGGTGAATTAC 121  
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122 AGGTGTGATCTTCCAAAGTGAATCCGTCGAGGAGAAATGATCTCCGAGTGGTGA 181  
186 GACGACACTGTCTCTGTCAGTGTCTCTTCTGTCAGTGTCCAGTGTCCAGGAGGCA 245  
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842 CGAGAGAGACCGATCAACCGCAGGTATGAGAGTCCAGGCTCCAGGCTCCAGAG 901  
906 CTTGACATCACTCTCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 965  
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1806 TGTGATATGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 1865  
1802 TGTGATATGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 1861  
1866 GGTGATATGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 1925  
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1926 GGTGATATGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 1985  
1922 GGTGATATGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 1981  
1986 TGTGATATGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 2045  
1982 TGTGATATGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACT 2041

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Db	2042	CTCTTGTCTTCTGGACCTTCCAGCTGTGCTCTCTACCTTTTACAGCATCATCTTC	2101
Qy	2106	CTTTCAGGCTTCTCTCATCTTCACTCTGTGTCTCATATGGGCTGAGGCCCCGGGTGG	2165
Db	2102	CTTTCAGGCTTCTCTCATCTTCACTCTGTGTCTCATATGGGCTGAGGCCCCGGGTGG	2161
Qy	2166	CCCCCTCCCTCTGAAAGAGCAACTCAGACTGCGCCAGGCTCCCATCAGCTCGGAGAC	2225
Db	2162	CCCCCTCCCTCTGAAAGAGCAACTCAGAGGGCCAGGCTCCCATCAGCTCGGAGAC	2221
Qy	2226	CTGCTCAAGCCGCACTTAAAGCTTCCAGCCCACTGCCCCATGTATTAAGAGATGACGG	2285
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Qy	2286	CTGTGTCGCAACATGCGCTGTGCCCCCGAGCCAGGCCAGGCCCAAGTCAAGCCGA	2345
Db	2282	CTGTGTCGCAACATGCGCTGTGCCCCCGAGCCAGGCCCAAGTCAAGTCAAGCCGA	2341
Qy	2346	GACTTTGGAAAGCCCAAGACCATGAGAGATGGGCGTTGCAATGGTGAACGGACTCC	2405
Db	2342	GACTTTGGAAAGCCCAAGACCATGAGAGATGGGCGTTGCAATGGTGAACGGACTCC	2401
Qy	2406	GGGGCTGGGGCTTTTGAATTTGGCCTTGGGGGACTACTGGCTCTCACTCAGTCCCAAGG	2465
Db	2402	GGG - CTGGGCTTTTGAATTTGGCCTTGGGGGACTACTGGCTCTCACTCAGTCCCAAGG	2459
Qy	2466	ACTCAGAAGTGGCGCCGCAATGTGCTTAAAGGATCTGTCCCAATCTGTCCCAACCCAGC	2525
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Qy	2526	TGAGAGCTGTGCTCTCTCCCTTACAACCCTGGGCGCAG - CTTCAATTGCTGGGGCCAGGCC	2584
Db	2520	TGAGAGCTGTGCTCTCTCCCTTACAACCCTGGGCGCAGCTCAATTGCTGGGGCCAGGCC	2579
Qy	2585	TTGGATCTTTAGAGGTCGTGGCAATCTCTTAATCTGTGCCCCCTGCTGGGAGACAGAAATGTG	2644
Db	2580	TTGGATCTTTAGAGGTCGTGGCAATCTCTTAATCTGTGTGCCCTGCTGGGAGACAGAAATGTG	2639
Qy	2645	GCTCAAGTTGCTCTGTCTCTCGTGTGTCAACCTGAGGGGCACTGTGATCTCTGTCAATTT	2704
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Db	2700	AACTTCAGGTGGACCCCAAGGGGAAATGGGGCCCAAGGGCAACCTTCAGGGCCAGACCTT	2759
Qy	2765	GGCGAGAGAGAGGCCCTTTTCCAGAGACACAGACAGTCTGCTTAACCTCTGAAGCC	2821
Db	2760	GGCGAGAGAGAGGCCCTTTTCCAGAGAGACACAGACAGTCTGCTTAACCTCTGAAGCC	2816

Search completed: February 12, 2005, 14:10:38  
Job time : 12130 secs





identified by the method of the invention, is useful as an appetite control agent for controlling appetite in an individual. The dominant negative mutant of GPR56 is useful for evaluating the role of GPR56 in the control of appetite. A transgenic non-human animal containing the GPR56 gene is useful for evaluating the effects of test compounds in appetite control and obesity. The agonists or antagonists of GPR56 are useful as appetite control agents for controlling obesity. AON is also useful as an appetite control agent. This polynucleotide sequence CC represents the cDNA of the human G protein-coupled receptor, GPR56, of the invention

Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;

Query Match 100.0%; Score 2822; DB 6; Length 2822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB CGTAACTCCACCTCCGGGTTCAAGTATTCATGCTCAGCTCCGAGTAGTGG 120
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DB 361 GTCCATGCCCCCTTCCCTGAGAGCCACCTGCTCCGATCTCCCTGACCCGAGGAG 420
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DB 421 CTCTACCACTTCTGCTCTACTGTGAGACGACATGCTGGAGATTAATCTTCTATG 480
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DB 481 AAGCTGATCTTCTGTGAGTGAACAAAGCTCTAGCTCTCTCTCTCTCTCTCTCTCT 540
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DB 721 AGCCAGTTCTGAGAGATCCCAAGAGGCTCAAGAGAGGCTTGGGCTGCCCGCAGC 780
QY 781 CAGCAGTTGACAGAGCTGAGTGCAGAACTGATCTGTGAGATTCATGGGAGACATGGTG 840
DB 781 CAGCAGTTGACAGAGCTGAGTGCAGAACTGATCTGTGAGATTCATGGGAGACATGGTG 840
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DB 841 TCCTTGAGAGAGACCGGATCAACGCCACGATGTGAAGCTTCAAGCCCAAGCCGCGCTC 900
QY 901 CAGACCTTCATTCACATCCCGGAGAGAGAGAGACAGAGAGATCATGAGTACTG 960
DB 901 CAGACCTTCATTCACATCCCGGAGAGAGAGAGAGAGAGAGATCATGAGTACTG 960
QY 961 GTGCTGCTCTCTGACATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GTGCTGCTCTCTGACATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 AAGCTCTCTCTGTGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 AAGCTCTCTCTGTGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 GTCTGAGTGAAGAGCTTGGGAGATTTGTGATACAGAACCAAGATGACCACTTCA 1140
DB 1081 GTCTGAGTGAAGAGCTTGGGAGATTTGTGATACAGAACCAAGATGACCACTTCA 1140
QY 1141 GAGCCGCTGTGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 GAGCCGCTGTGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 GTGTTCTGTGATGAAGACCCCAATTTGATGATGATGATGATGATGATGATGAT 1260
DB 1201 GTGTTCTGTGATGAAGACCCCAATTTGATGATGATGATGATGATGATGATGAT 1260
QY 1261 GAGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 GAGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 GTGCTGATGATCTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 GTGCTGATGATCTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 TCCATGATGATCTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 TCCATGATGATCTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 TGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 TGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 ATGAACTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 ATGAACTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 GGCCTGACAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 GGCCTGACAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 CTGACCTGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 CTGACCTGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 GTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 GTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CCAATCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 CCAATCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 TTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1801 TTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1861 TTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 TTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GCAATGCTAGACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
DB 1921 GCAATGCTAGACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
```

[illegible]

XX		Human; GPR22; anorectic; appetite control agent; GPR; gene;
KM	G protein-coupled receptor; orphan receptor; antisense gene therapy;	
KM	mouse; GPR56; ds.	
XX		
OS	Homo sapiens.	
XX		
FN	WO200183550-A2.	
XX		
PD	08-NOV-2001.	
PF	30-APR-2001; 2001WO-GB001874.	
XX		
PR	03-MAY-2000; 2000US-0201418P.	
XX		
PA	(ASTR ) ASTRAZENCA AB.	
PA	(ASTR ) ASTRAZENCA UK LTD.	
XX		
PI	Brennand JC, Hart KA;	
DR	WPI; 2002-066519/09.	
XX		
PT	Identifying appetite control agent for controlling obesity, comprises screening agonists or antagonists of G protein-coupled receptor, GPR22, and using them as test compounds in appetite control test procedures.	
PS	Claim 6; Page 18-19; 21pp; English.	
XX		
CC	The invention relates to identifying an anorectic appetite control agent, comprising screening for agonists and/or antagonists of G protein-coupled receptor GPR22 (an orphan receptor), using one or more agonists and/or antagonists so identified as test compounds in one or more appetite control procedures and selecting an active compound for use as an appetite control agent. An antisense oligonucleotide to the GPR22 gene is also useful for controlling obesity using antisense gene therapy. Note: The GPR22 encoding cDNA sequence (ABA05328) and encoded protein (ABA05329) are disclosed, however two DNA sequences described as human (ABA05329) and mouse (ABA05328) GPR56 are given in the sequence listing , but are not otherwise referred to in the specification	
XX		
SQ	Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 2822; DB 6; Length 2822;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGGACAGCAGGGGTCTCGCTCTGTACAACAAGCTGAAGTGCATGTTGATCTTGCTCAT	60
DB	1 CGGACAGCAGGGGTCTCGCTCTGTACAACAAGCTGAAGTGCATGTTGATCTTGCTCAT	60
QY	61 CTGAACCTCACTCCCGGGGTCAAGTAGATTCTAATGGCTGACCTCCCGAGTAGCTGG	120
DB	61 CTGAACCTCACTCCCGGGGTCAAGTAGATTCTAATGGCTGACCTCCCGAGTAGCTGG	120
QY	121 ATTAACAGGTGTGACTTTCAGAAGTGACTCCGTGGAAGAAATGACTGCCAGTGCCTG	180
DB	121 ATTAACAGGTGTGACTTTCAGAAGTGACTCCGTGGAAGAAATGACTGCCAGTGCCTG	180
QY	181 CTGCAGACGACACTGTGTTCTCTGTAAGTCTGCTCTTCTTGSTGCCAAGGTGCCACGGCAGS	240
DB	181 CTGCAGACGACACTGTGTTCTCTGTAAGTCTGCTCTTCTTGSTGCCAAGGTGCCACGGCAGS	240
QY	241 GGCCACAGGGGAAGACTTTGCTTCTGCACCGCAGCGGAACAGACACACAGAGACAGCTTC	300
DB	241 GGCCACAGGGGAAGACTTTGCTTCTGCACCGCAGCGGAACAGACACACAGAGACAGCTTC	300
QY	301 CACTACAAACCACACACAGACTGCGCATCTCATATGAATCTCCGAAGAAGGCGCTCAC	360
DB	301 CACTACAAACCACACACAGACTGCGCATCTCATATGAATCTCCGAAGAAGGCGCTCAC	360
QY	361 GTCCATGCCCCCTTCCCTGACGCCAACCCGACTTCCCGATCTTCCCTGACCCGAGGGC	420
DB	361 GTCCATGCCCCCTTCCCTGACGCCAACCCGACTTCCCGATCTTCCCTGACCCGAGGGC	420

Oy	421	CTCTAACCACTTCTGECTCTCTACTGGAACCCGACATATGCTGGAGATTACATCTTCTCTATGGC	480
Db	421	CTTACACACTTCTGECTCTCTACTGGAACCGACATATGCTGGAGATTACATCTTCTCTATGGC	480
Oy	481	AAGGTGACCTTCTTGCTGATGAGCAAAAGCCTTAGCTCTCTGCTTCCAGACACAGAG	540
Db	481	AAGGTGACTTCTTGCTGATGAGCAAAAGCCTTAGCTCTCTGCTTCCAGACACAGAG	540
Oy	541	GAGAGCCTGAGTCAAGGAGCCCGGCTGTTAGCCACTTCTGTCACTCTCTGATGAGCCCT	600
Db	541	GAGAGCCTGAGTCAAGGAGCCCGGCTGTTAGCCACTTCTGTCACTCTCTGATGAGCCCT	600
Oy	601	CAGAAACATACAGCTGCCAGTGGCCGACGACTTACCTTCTCCCTTCCAGTCCGCCAC	660
Db	601	CAGAAACATACAGCTGCCAGTGGCCGACGACTTACCTTCTCCCTTCCAGTCCGCCAC	660
Oy	661	ACGGCCGCTCAAAATGCTCTGGTGGACATATGTCGAGCTCAAAAGGACCTTCAGCTGCTC	720
Db	661	ACGGCCGCTCAAAATGCTCTGGTGGACATATGTCGAGCTCAAAAGGACCTTCAGCTGCTC	720
Oy	721	AGCCAGTTCTCGAAGCATCCCGCAAAAGGCTTCAGAGAGGCTCTGGCTGGCCCGCCAGC	780
Db	721	AGCCAGTTCTCGAAGCATCCCGCAAAAGGCTTCAGAGAGGCTCTGGCTGGCCCGCCAGC	780
Oy	781	CAGCAGTTGCAGAGCTGTGAGATCGAAACTGTGAGATTCAATGGGGGACATGTTG	840
Db	781	CAGCAGTTGCAGAGCTGTGAGATCGAAACTGTGAGATTCAATGGGGGACATGTTG	840
Oy	841	TCCTTTCAGAGAGACCGGATCAACGCCACGGTATGAAAGCTCCAGCCCAAGCTGGCTC	900
Db	841	TCCTTTCAGAGAGACCGGATCAACGCCACGGTATGAAAGCTCCAGCCCAAGCTGGCTC	900
Oy	901	CAGGACCTGCACATCCACATCCCGGAGAGGAGAGACAGAGCATATGGAATATCTG	960
Db	901	CAGGACCTGCACATCCACATCCCGGAGAGGAGAGACAGAGCATATGGAATATCTG	960
Oy	961	GTGCTGCTGCTCGAACACTCTTCCAGAGAGCAGAAAGGCCGAGCCGGAGAGCTGAGAG	1020
Db	961	GTGCTGCTGCTCGAACACTCTTCCAGAGAGCAGAAAGGCCGAGCCGGAGAGCTGAGAG	1020
Oy	1021	AGACCTCCCTCTGTGGACTTTCAGAGACCAACCCCTTCCAGAGCAAGAAATTCAGAGCA	1080
Db	1021	AGACCTCCCTCTGTGGACTTTCAGAGACCAACCCCTTCCAGAGCAAGAAATTCAGAGCA	1080
Oy	1081	GTCTGTGGTGAAGAGTCTTGGGGATTGTGGTACAGAACCAACAGTAGACCAACTCAGC	1140
Db	1081	GTCTGTGGTGAAGAGTCTTGGGGATTGTGGTACAGAACCAACAGTAGACCAACTCAGC	1140
Oy	1141	GAGCCCGTGTGTCTCACTTTCAGACACAAGCTACAGCCGAGAAATGTATCTGTCAATGT	1200
Db	1141	GAGCCCGTGTGTCTCACTTTCAGACACAAGCTACAGCCGAGAAATGTATCTGTCAATGT	1200
Oy	1201	GTGTTCTGGGTTGAAGACCCCAATTGAGACGCCCGGGGACATTGGAGCAGTGTGGGTGT	1260
Db	1201	GTGTTCTGGGTTGAAGACCCCAATTGAGACGCCCGGGGACATTGGAGCAGTGTGGGTGT	1260
Oy	1261	GAGACCGTCAAGAGAGAAACCAACATCTGTCTTTCGAAACCACTTAGCTTACTTTCGA	1320
Db	1261	GAGACCGTCAAGAGAGAAACCAACATCTGTCTTTCGAAACCACTTAGCTTACTTTCGA	1320
Oy	1321	GTGCTGATGTGTCTCTGGTGGAGGTGAGACCGGTGACAAAGCACTATCAGAGCTCTCTC	1380
Db	1321	GTGCTGATGTGTCTCTGGTGGAGGTGAGACCGGTGACAAAGCACTATCAGAGCTCTCTC	1380
Oy	1381	TCCTTACGTGGGCTGTGTGTCTCTGCTCCGCTGAGCTTGTTCACCAATTCGCGCTCACTC	1440
Db	1381	TCCTTACGTGGGCTGTGTGTCTCTGCTCCGCTGAGCTTGTTCACCAATTCGCGCTCACTC	1440
Oy	1441	TGCTTCAAGGTGTCCCTGTGCTGAGAGAGAAACCTCGGACTTACACATATGAGGTGAC	1500
Db	1441	TGCTTCAAGGTGTCCCTGTGCTGAGAGAGAAACCTCGGACTTACACATATGAGGTGAC	1500

QY	1501	ATGAACCTGCTGCTGGCCGCTCTTCCCTGCTGGAACAAGAGTTTCCTGTCAGAGGACGGG	1560
Db	1501	ATGAACCTGCTGCTGGCCGCTCTTCCCTGCTGGAACAAGAGTTTCCTGTCAGAGGACGGG	1560
QY	1561	GCCCTGACAGAGCTCTGAGGCTGAGCTCCAGACCAAGTGCACATCTTCCTGACCTTCCCTG	1620
Db	1561	GCCCTGACAGAGCTCTGAGGCTGAGCTCCAGACCAAGTGCACATCTTCCTGACCTTCCCTG	1620
QY	1621	CTGACCTGCTCTTCTGGAATGGGCTCTGAGGGGTACAACCTCTACCGATCTCGTGGTGGAG	1680
Db	1621	CTGACCTGCTCTTCTGGAATGGGCTCTGAGGGGTACAACCTCTACCGATCTCGTGGTGGAG	1680
QY	1681	GTCTTTGGGACCTATGTCCTGGGCTACACTGACCTGAGCGGCAATGGGCTTGGGCTTTC	1740
Db	1681	GTCTTTGGGACCTATGTCCTGGGCTACACTGACCTGAGCGGCAATGGGCTTGGGCTTTC	1740
QY	1741	CCCATCTTTCCTGTGACGCTGTGGCCCTGGTGAATGTGACCACTATGCCCCCATATC	1800
Db	1741	CCCATCTTTCCTGTGACGCTGTGGCCCTGGTGAATGTGACCACTATGCCCCCATATC	1800
QY	1801	TTGGCTGTGGATAGGAATCCAGAGGGGCTCATCTACCTTCCATGTGCTGATATCCGGAGAC	1860
Db	1801	TTGGCTGTGGATAGGAATCCAGAGGGGCTCATCTACCTTCCATGTGCTGATATCCGGAGAC	1860
QY	1861	TCCCTGTGAGCTACATACACAACCTGGGCTCTTCCAGCTGTGTCTTCTTCAACATG	1920
Db	1861	TCCCTGTGAGCTACATACACAACCTGGGCTCTTCCAGCTGTGTCTTCTTCAACATG	1920
QY	1921	GCCATGCTAGCGACCAATGCTGTGTGACAAATCTCTGCGCTGGGCGCCCAACCCAAAAGTG	1980
Db	1921	GCCATGCTAGCGACCAATGCTGTGTGACAAATCTCTGCGCTGGGCGCCCAACCCAAAAGTG	1980
QY	1981	TCACATGTGCTGACACTGCTGAGGCGCTGAGCTGTGCTTGGGCTGTGCGCTTGGGCTTGATC	2040
Db	1981	TCACATGTGCTGACACTGCTGAGGCGCTGAGCTGTGCTTGGGCTGTGCGCTTGGGCTTGATC	2040
QY	2041	TTCTTCTCTCTTGTGCTTGTGGAACCTTCCAGCTTGTGCTCTTCACTCTTTGAGACATATC	2100
Db	2041	TTCTTCTCTCTTGTGCTTGTGGAACCTTCCAGCTTGTGCTCTTCACTCTTTGAGACATATC	2100
QY	2101	ACCTCTCTCCAGAGGCTTCTCATCTTTCATCTGTGATCTGTGTCATGCGGCTGACAGGCGCG	2160
Db	2101	ACCTCTCTCCAGAGGCTTCTCATCTTTCATCTGTGATCTGTGTCATGCGGCTGACAGGCGCG	2160
QY	2161	GGTGGCCCCCTCCCTCTGGAAGCAACTGAGCTGCGCCAGGCTCCCATACAGCTGGGCT	2220
Db	2161	GGTGGCCCCCTCCCTCTGGAAGCAACTGAGCTGCGCCAGGCTCCCATACAGCTGGGCT	2220
QY	2221	AGCACTGTGTCAAGCCGCACTTAGGCTTCCAGCCCACTGCGCATGTGATGAGACAGAGA	2280
Db	2221	AGCACTGTGTCAAGCCGCACTTAGGCTTCCAGCCCACTGCGCATGTGATGAGACAGAGA	2280
QY	2281	TGCGGCTCTGTGCAACTGTGCTGTGGCCGCCGAGCCAGGCGCCACAGGCGCAGTGAG	2340
Db	2281	TGCGGCTCTGTGCAACTGTGCTGTGGCCGCCGAGCCAGGCGCCACAGGCGCAGTGAG	2340
QY	2341	CCGCAGACTTTGGAAGGCCCAACGACCATGAGAGATGGGCGCTTTGGCAATGTGGAGACGA	2400
Db	2341	CCGCAGACTTTGGAAGGCCCAACGACCATGAGAGATGGGCGCTTTGGCAATGTGGAGACGA	2400
QY	2401	CTCCCGGAGGCTGGGCTTTTGAATTGGCTTGGGGAATTAAGCTGAGCTCTCACTCACTGCC	2460
Db	2401	CTCCCGGAGGCTGGGCTTTTGAATTGGCTTGGGGAATTAAGCTGAGCTCTCACTCACTGCC	2460
QY	2461	ACGGGACTTCAGAAATGGCGCGCATGCTGCTTGAAGGTATGTCCCCCAATCTGTGCCAAC	2520
Db	2461	ACGGGACTTCAGAAATGGCGCGCATGCTGCTTGAAGGTATGTCCCCCAATCTGTGCCAAC	2520
QY	2521	CCAGGCTGAGAGGCTGAGTCTCTCTTCAACCCCTGGGCGCCAGGCTCATATGCTGGGGGCGCA	2580
Db	2521	CCAGGCTGAGAGGCTGAGTCTCTCTTCAACCCCTGGGCGCCAGGCTCATATGCTGGGGGCGCA	2580
QY	2581	GGCCTTGAATCTTGAAGGCTTGGGCAATCTTAAATCTGTGCCCCCTGCTGGGACAGAAA	2640

DB 2581 GGCCTTGAATCTTGAAGGCTGGACATCTTAACTCTGTGCCCTGGAGCAGAAA 2640  
 QY 2641 TGTGGCTCCAGTGTCTGTCTCTCGTGTACCCCTGAGGGCACTGTGATCTCTGTCA 2700  
 DB 2641 TGTGGCTCCAGTGTCTGTCTCTCGTGTACCCCTGAGGGCACTGTGATCTCTGTCA 2700  
 QY 2701 TTTTAACTTCAAGTGTGACCCAGAGGGCGAATGGGGCCAGAGGCACTTCAAGGGCCAGAG 2760  
 DB 2701 TTTTAACTTCAAGTGTGACCCAGAGGGCGAATGGGGCCAGAGGCACTTCAAGGGCCAGAG 2760  
 QY 2761 CCTTGGCGAGAGAGAGGCGCTTTTCCAGAGACAGAGAGAGAGCTGCTTCACTTCAAGCC 2820  
 DB 2761 CCTTGGCGAGAGAGAGGCGCTTTTCCAGAGACAGAGAGAGAGCTGCTTCACTTCAAGCC 2820  
 QY 2821 CG 2822  
 DB 2821 CG 2822  
 DB 2821 CG 2822

## RESULT 3

AB242865  
 ID AB242865 standard; DNA; 2822 BP.

XX AB242865;

XX 04-MAR-2003 (first entry)

DE Human G protein-coupled receptor TM7XN1/GPR56 DNA SEQ ID NO:517.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KM G protein-coupled receptor modulator; antibody; immune-related disease;  
 KM growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KM immunological-related cell proliferative disease; autoimmune disease;  
 KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KM osteoporosis; host disease; Parkinson's disease; multiple sclerosis; pain;  
 KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KM ulcer; gene; ds.

XX Homo sapiens.

XX MO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX P-PSDB; ABP82015.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.

XX Disclosure: Fig 1; 523bp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an

CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242865 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention

XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 2822; DB 8; Length 2822;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGAGAGGGTCTCGCTCTGTGACACAGAGCTGAGAGTGTGATCTTGGCTCAT 60  
 DB 1 CGGCGAGAGGGTCTCGCTCTGTGACACAGAGCTGAGAGTGTGATCTTGGCTCAT 60  
 QY 61 CGTAACTTCAACCTCCCGGGGTTCAAGTATCTCATGCTTCAAGCTCCCGAGTACTGGG 120  
 DB 61 CGTAACTTCAACCTCCCGGGGTTCAAGTATCTCATGCTTCAAGCTCCCGAGTACTGGG 120  
 QY 61 ATTACAGGTGTGATCTTCAAGAGTACTCCGTGAGAGAAATGATCTCCCAAGTGGCTG 180  
 DB 61 ATTACAGGTGTGATCTTCAAGAGTACTCCGTGAGAGAAATGATCTCCCAAGTGGCTG 180  
 QY 121 ATTACAGGTGTGATCTTCAAGAGTACTCCGTGAGAGAAATGATCTCCCAAGTGGCTG 180  
 DB 121 ATTACAGGTGTGATCTTCAAGAGTACTCCGTGAGAGAAATGATCTCCCAAGTGGCTG 180  
 QY 181 CTGCAAGACGACATGTTCTCTGCTAGTCTCTTCTTCTGCTCAAGAGTGGCCACGAGCAG 240  
 DB 181 CTGCAAGACGACATGTTCTCTGCTAGTCTCTTCTTCTGCTCAAGAGTGGCCACGAGCAG 240  
 QY 181 CTGCAAGACGACATGTTCTCTGCTAGTCTCTTCTTCTGCTCAAGAGTGGCCACGAGCAG 240  
 DB 181 CTGCAAGACGACATGTTCTCTGCTAGTCTCTTCTTCTGCTCAAGAGTGGCCACGAGCAG 240  
 QY 241 GGGCGAGAGGAAAGATTCTGCTTGCAGCCAGCGGAAACACACACAGAGAGCCTTC 300  
 DB 241 GGGCGAGAGGAAAGATTCTGCTTGCAGCCAGCGGAAACACACACAGAGAGCCTTC 300  
 QY 301 CACTACAAACCCACACACAGACTGTGCTTCATATGAGAACTCCGAAAGAGGCTTCACA 360  
 DB 301 CACTACAAACCCACACACAGACTGTGCTTCATATGAGAACTCCGAAAGAGGCTTCACA 360  
 QY 301 CACTACAAACCCACACACAGACTGTGCTTCATATGAGAACTCCGAAAGAGGCTTCACA 360  
 DB 301 CACTACAAACCCACACACAGACTGTGCTTCATATGAGAACTCCGAAAGAGGCTTCACA 360  
 QY 361 GTCCATGCCCCCTTCCCTGAGAGCCACCTGCTCCGATCCCTGAGCCCGAGGAGC 420  
 DB 361 GTCCATGCCCCCTTCCCTGAGAGCCACCTGCTCCGATCCCTGAGCCCGAGGAGC 420  
 QY 361 GTCCATGCCCCCTTCCCTGAGAGCCACCTGCTCCGATCCCTGAGCCCGAGGAGC 420  
 DB 361 GTCCATGCCCCCTTCCCTGAGAGCCACCTGCTCCGATCCCTGAGCCCGAGGAGC 420  
 QY 421 CTCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGATTAATCTTCTTATGGC 480  
 DB 421 CTCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGATTAATCTTCTTATGGC 480  
 QY 421 CTCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGATTAATCTTCTTATGGC 480  
 DB 421 CTCTACCACTTCTGCTCTACTGAAACCGACATGCTGAGATTAATCTTCTTATGGC 480  
 QY 481 AAGCGTGAATTTTCTGAGTGAACAAAGCTTCTTCTGCTTCTGCTTCAAGACAGAG 540  
 DB 481 AAGCGTGAATTTTCTGAGTGAACAAAGCTTCTTCTGCTTCTGCTTCAAGACAGAG 540  
 QY 481 AAGCGTGAATTTTCTGAGTGAACAAAGCTTCTTCTGCTTCTGCTTCAAGACAGAG 540  
 DB 481 AAGCGTGAATTTTCTGAGTGAACAAAGCTTCTTCTGCTTCTGCTTCAAGACAGAG 540  
 QY 541 GAGAGCTGGCTCAAGAGGCCCCCGCTTTAGGCACTTGTCACTCTCGTGAAGCCCT 600  
 DB 541 GAGAGCTGGCTCAAGAGGCCCCCGCTTTAGGCACTTGTCACTCTCGTGAAGCCCT 600  
 QY 541 GAGAGCTGGCTCAAGAGGCCCCCGCTTTAGGCACTTGTCACTCTCGTGAAGCCCT 600  
 DB 541 GAGAGCTGGCTCAAGAGGCCCCCGCTTTAGGCACTTGTCACTCTCGTGAAGCCCT 600  
 QY 601 CAGAAATCAGCTGCTCCAGAGTCCGAGCTTCACTTCTCTTCAAGTCTTCCCGAC 660  
 DB 601 CAGAAATCAGCTGCTCCAGAGTCCGAGCTTCACTTCTCTTCAAGTCTTCCCGAC 660  
 QY 601 CAGAAATCAGCTGCTCCAGAGTCCGAGCTTCACTTCTCTTCAAGTCTTCCCGAC 660  
 DB 601 CAGAAATCAGCTGCTCCAGAGTCCGAGCTTCACTTCTCTTCAAGTCTTCCCGAC 660  
 QY 661 AGGCGCTGACAAATCCCTCGGTGACATGTCGAGACTCAAAAGGACCTCCAGTGGCTC 720  
 DB 661 AGGCGCTGACAAATCCCTCGGTGACATGTCGAGACTCAAAAGGACCTCCAGTGGCTC 720  
 QY 661 AGGCGCTGACAAATCCCTCGGTGACATGTCGAGACTCAAAAGGACCTCCAGTGGCTC 720  
 DB 661 AGGCGCTGACAAATCCCTCGGTGACATGTCGAGACTCAAAAGGACCTCCAGTGGCTC 720

QY 721 AGCCAGTTCTGAAGCATCCCAAGAGGCTTCAAGAGGCTCTGAGCTGCCCCCGCAGC 780  
DB 721 AGCCAGTTCTGAAGCATCCCAAGAGGCTTCAAGAGGCTCTGAGCTGCCCCCGCAGC 780  
QY 781 CAGCAGTTGCAAGAGGCTGAGAGTGAATCTGACCTCTGTGAGATTCAAGAGGAGCATGAGT 840  
DB 781 CAGCAGTTGCAAGAGGCTGAGAGTGAATCTGACCTCTGTGAGATTCAAGAGGAGCATGAGT 840  
QY 841 TCCCTGAGAGAGAGCCGGATCAACGCCAGGTATGAAAGCTTCAAGCCCAAGCCGAGCTC 900  
DB 841 TCCCTGAGAGAGAGCCGGATCAACGCCAGGTATGAAAGCTTCAAGCCCAAGCCGAGCTC 900  
QY 901 CAGAGCTTGCACATCCACTCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
DB 901 CAGAGCTTGCACATCCACTCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
QY 961 GTGCTGCTGCTGCAACATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
DB 961 GTGCTGCTGCTGCAACATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1021 AGACTCTCTCTGAGTGAATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
DB 1021 AGACTCTCTCTGAGTGAATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
QY 1081 GTCTGAGTGAAGAGGCTTGGAGATTTGTGTATCAAGAACCAAGATGAGAGAGAGAGAG 1140  
DB 1081 GTCTGAGTGAAGAGGCTTGGAGATTTGTGTATCAAGAACCAAGATGAGAGAGAGAGAG 1140  
QY 1141 GAGCCGCTGAGTCACTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
DB 1141 GAGCCGCTGAGTCACTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
QY 1201 GTGTTCTGGGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
DB 1201 GTGTTCTGGGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
QY 1261 GAGAGCGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320  
DB 1261 GAGAGCGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320  
QY 1321 GTGCTGAGTGTCTCTCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
DB 1321 GTGCTGAGTGTCTCTCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
QY 1381 TCCCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
DB 1381 TCCCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
QY 1441 TGCTCAAGAGTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
DB 1441 TGCTCAAGAGTGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
QY 1501 ATGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560  
DB 1501 ATGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560  
QY 1561 GCGCTGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
DB 1561 GCGCTGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
QY 1621 CTCACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
DB 1621 CTCACTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680  
QY 1681 GTCTTTGGCAGTATGTCTCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
DB 1681 GTCTTTGGCAGTATGTCTCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740  
QY 1741 CCATCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
DB 1741 CCATCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
QY 1801 TTGGCTGTGATGAGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860

DB 1801 TTGGCTGTGATGAGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
QY 1861 TCCCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920  
DB 1861 TCCCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920  
QY 1921 GCCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
DB 1921 GCCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
QY 1981 TCAATGTGTGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
DB 1981 TCAATGTGTGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
QY 2041 TTCTTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100  
DB 2041 TTCTTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100  
QY 2101 ACCCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
DB 2101 ACCCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160  
QY 2161 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
DB 2161 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
QY 2221 AGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280  
DB 2221 AGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280  
QY 2281 TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
DB 2281 TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
QY 2341 CCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
DB 2341 CCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
QY 2401 CTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460  
DB 2401 CTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460  
QY 2461 ACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
DB 2461 ACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520  
QY 2521 CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
DB 2521 CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
QY 2581 GAGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640  
DB 2581 GAGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640  
QY 2641 TGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700  
DB 2641 TGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2700  
QY 2701 TTTTAACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
DB 2701 TTTTAACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
QY 2761 CCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
DB 2761 CCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
QY 2821 CG 2822  
DB 2821 CG 2822

RESULT 4



ADAI4217  
 ID ADAI4217 standard; cDNA; 2822 BP.  
 AC ADAI4217;  
 XX  
 XX  
 DT 06-NOV-2003 (first entry)  
 DE Human GPR56-1 encoding cDNA SEQ ID NO:1.  
 XX  
 XX human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;  
 KM GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;  
 XX gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 163..2244  
 FT /\*tag= a  
 FT /product= "GPR56-1"  
 XX  
 XX MO2003068965-A1.  
 XX  
 XX 21-AUG-2003.  
 XX  
 XX 12-FEB-2003; 2003MO-AU000178.  
 XX  
 XX 12-FEB-2002; 2002US-00073054.  
 XX  
 XX (GTWO-) G2 THERAPIES LTD.  
 XX  
 XX Herzog H, Sutherland RL, Mackay CR, Heneshall S;  
 DR WPI, 2003-689676/65.  
 DR P-PSDB; ADAI4218.  
 XX  
 XX New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.  
 PT  
 XX  
 XX Claim 1; Page 88-92; 129pp; English.  
 XX  
 XX The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumor growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytostatic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumor growth. The present sequence encodes the human GPCR,  
 CC designated GPR56-1, which is used in the exemplification of the present  
 CC invention.  
 XX  
 XX  
 SQ Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 2822; DB 9; Length 2822;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGGACGACAGGCTCTGCTGTCACACAGGCTGAGTGCAGTGTGTGATCTTGGTCAAT 60  
 DB 1 CGGACGACAGGCTCTGCTGTCACACAGGCTGAGTGCAGTGTGTGATCTTGGTCAAT 60  
 QY 61 CGTAACTTCACCTCCCGGCTTCAAGTATCTCATGCTTCAGCCTCCCGAGTAGCTGGG 120  
 DB 61 CGTAACTTCACCTCCCGGCTTCAAGTATCTCATGCTTCAGCCTCCCGAGTAGCTGGG 120  
 QY 121 ATTACAGTGTGATCTTCCAAAGATGATCTCCGTGGAGGAAATGACTCCCGATGCGTG 180  
 DB 121 ATTACAGTGTGATCTTCCAAAGATGATCTCCGTGGAGGAAATGACTCCCGATGCGTG 180

DB 121 ATTACAGTGTGATCTTCCAAAGATGATCTCCGTGGAGGAAATGACTCCCGATGCGTG 180  
 QY 181 CTGACAGACGACTGTCTCTGCTGAGTGTGCTCTTCTGCTCAAGTCCCAAGCGCAGG 240  
 DB 181 CTGACAGACGACTGTCTCTGCTGAGTGTGCTCTTCTGCTCAAGTCCCAAGCGCAGG 240  
 QY 241 GGGCACAAGGAAAGACTTTGCTTCTGACAGCAGCGGAAACCAACACACAGGACAGCTC 300  
 DB 241 GGGCACAAGGAAAGACTTTGCTTCTGACAGCAGCGGAAACCAACACACAGGACAGCTC 300  
 QY 301 CACTAACAACCCACACACAGCCTGGCATCTTCATGAGAGACTCCGAGAGGCTCACA 360  
 DB 301 CACTAACAACCCACACACAGCCTGGCATCTTCATGAGAGACTCCGAGAGGCTCACA 360  
 QY 361 GTCCATGCCCTTTCCCTGAGGCCAACCTGCTTCCGATCTTCCCTGACCCCAAGGGGC 420  
 DB 361 GTCCATGCCCTTTCCCTGAGGCCAACCTGCTTCCGATCTTCCCTGACCCCAAGGGGC 420  
 QY 421 CTCTACCACTTGTGCTCTTCTGAGAACCCGACATGCTGGGAGATTACATCTTCTTAAGC 480  
 DB 421 CTCTACCACTTGTGCTCTTCTGAGAACCCGACATGCTGGGAGATTACATCTTCTTAAGC 480  
 QY 481 AAGGTGACCTTCTTGTGAGTGAACAAGCTCTAGCTCTCTGCTTCCAGCACAGAG 540  
 DB 481 AAGGTGACCTTCTTGTGAGTGAACAAGCTCTAGCTCTCTGCTTCCAGCACAGAG 540  
 QY 541 GAGAGCTGTGCTCAGGGCCCCCGCTGTAGCCACTTCTGTACCTCTGTGTGAGAGCCT 600  
 DB 541 GAGAGCTGTGCTCAGGGCCCCCGCTGTAGCCACTTCTGTACCTCTGTGTGAGAGCCT 600  
 QY 541 GAGAGCTGTGCTCAGGGCCCCCGCTGTAGCCACTTCTGTACCTCTGTGTGAGAGCCT 600  
 DB 541 GAGAGCTGTGCTCAGGGCCCCCGCTGTAGCCACTTCTGTACCTCTGTGTGAGAGCCT 600  
 QY 601 CAGAACTACAGCTGCTCCCAAGTCCGACAGCTTCACTTCTTCCAGAGCTCTCCAC 660  
 DB 601 CAGAACTACAGCTGCTCCCAAGTCCGACAGCTTCACTTCTTCCAGAGCTCTCCAC 660  
 QY 601 CAGAACTACAGCTGCTCCCAAGTCCGACAGCTTCACTTCTTCCAGAGCTCTCCAC 660  
 DB 601 CAGAACTACAGCTGCTCCCAAGTCCGACAGCTTCACTTCTTCCAGAGCTCTCCAC 660  
 QY 661 ACGGCGCTGCAATGCTCGGTGAGACATGTGCGAGCTCAAAAGGAGCTTCAAGTCTC 720  
 DB 661 ACGGCGCTGCAATGCTCGGTGAGACATGTGCGAGCTCAAAAGGAGCTTCAAGTCTC 720  
 QY 721 AGCGATTCCTGAAGCATCTCCAGAAAGGCTTCAAGAGGCTTCCGCTGCTCCCGCCAGC 780  
 DB 721 AGCGATTCCTGAAGCATCTCCAGAAAGGCTTCAAGAGGCTTCCGCTGCTCCCGCCAGC 780  
 QY 721 AGCGATTCCTGAAGCATCTCCAGAAAGGCTTCAAGAGGCTTCCGCTGCTCCCGCCAGC 780  
 DB 721 AGCGATTCCTGAAGCATCTCCAGAAAGGCTTCAAGAGGCTTCCGCTGCTCCCGCCAGC 780  
 QY 781 CAGCAGTTGCAAGGCTGAGATCCGAAATGACCTTGTGAGATTATGAGGAGCAATG 840  
 DB 781 CAGCAGTTGCAAGGCTGAGATCCGAAATGACCTTGTGAGATTATGAGGAGCAATG 840  
 QY 841 TCCTTGAAGAGGACCGATCAACCGATGAGAAAGCTTCAAGCTCCAGCCGAGCTC 900  
 DB 841 TCCTTGAAGAGGACCGATCAACCGATGAGAAAGCTTCAAGCTCCAGCCGAGCTC 900  
 QY 901 CAGGACCTGACATCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
 DB 901 CAGGACCTGACATCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
 QY 901 CAGGACCTGACATCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
 DB 901 CAGGACCTGACATCTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
 QY 961 GTGCTGCTGCTTCCGAACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
 DB 961 GTGCTGCTGCTTCCGAACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
 QY 1021 AAGCTCTCTCTGTGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 DB 1021 AAGCTCTCTCTGTGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080  
 QY 1081 GTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 DB 1081 GTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 QY 1141 GAGCCGCTGCTGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
 DB 1141 GAGCCGCTGCTGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
 QY 1201 GTGCTTGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
 DB 1201 GTGCTTGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

Db 1201 GTGTTCTGGAGTTGAGAGCCCAATTGAGCAGCCCGGAGCAATTGAGAGAGTGTGGTGT 1260  
 QY 1261 GAGACCGTGAAGAGAGAGAAACCAACATCTGCTTGTGAAACCACTTGAACCTTATGCA 1320  
 Db 1261 GAGACCGTGAAGAGAGAGAAACCAACATCTGCTTGTGAAACCACTTGAACCTTATGCA 1320  
 QY 1321 GTGCTGATGATCTCTCTGAGTGAAGTGAACCGGTGCAACAGACCTTACCTGACCTTCTC 1380  
 Db 1321 GTGCTGATGATCTCTCTGAGTGAAGTGAACCGGTGCAACAGACCTTACCTGACCTTCTC 1380  
 QY 1381 TCTCTAGTGGGCTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
 Db 1381 TCTCTAGTGGGCTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
 QY 1441 TCTCTAGTGGGCTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 Db 1441 TCTCTAGTGGGCTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
 QY 1501 ATGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 Db 1501 ATGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
 QY 1561 GGCCTGACAGGCTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1620  
 Db 1561 GGCCTGACAGGCTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1620  
 QY 1621 CTACCTGCTCTTCTCTGATGAGGCTCTGAGGAGTGAACAACCTTACCGACTGTGTGTGAG 1680  
 Db 1621 CTACCTGCTCTTCTCTGATGAGGCTCTGAGGAGTGAACAACCTTACCGACTGTGTGTGAG 1680  
 QY 1681 GTCTTTGGGACCTTATGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
 Db 1681 GTCTTTGGGACCTTATGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
 QY 1741 CCCATCTTCTGTGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1800  
 Db 1741 CCCATCTTCTGTGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1800  
 QY 1801 TTGGCTGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1860  
 Db 1801 TTGGCTGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1860  
 QY 1861 TCCCTGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1920  
 Db 1861 TCCCTGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1920  
 QY 1921 GCCATGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1980  
 Db 1921 GCCATGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 1980  
 QY 1981 TCAATGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2040  
 Db 1981 TCAATGTGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2040  
 QY 2041 TTCTTCTCTTGTGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2100  
 Db 2041 TTCTTCTCTTGTGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2100  
 QY 2101 ACCCTCTTCAAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2160  
 Db 2101 ACCCTCTTCAAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2160  
 QY 2161 GGTGGGCTCTCTCTGAGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2220  
 Db 2161 GGTGGGCTCTCTCTGAGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2220  
 QY 2221 AGGACCTGTCTGAGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2280  
 Db 2221 AGGACCTGTCTGAGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2280  
 QY 2281 TGGGCTCTGTGAGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2340  
 Db 2281 TGGGCTCTGTGAGAGAGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2340

QY 2341 CCGCAGACTTTGAGAAAGCCCAACGACCATGAGAGAGTGGCCGTTGCCATGCTGTGAGCGGA 2400  
 Db 2341 CCGCAGACTTTGAGAAAGCCCAACGACCATGAGAGAGTGGCCGTTGCCATGCTGTGAGCGGA 2400  
 QY 2401 CTCCCGGGGCTGAGGCTTTTGAATTGGCTTGGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAG 2460  
 Db 2401 CTCCCGGGGCTGAGGCTTTTGAATTGGCTTGGAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAG 2460  
 QY 2461 ACAGGACTGAGAGTGGCGGCGCATGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAG 2520  
 Db 2461 ACAGGACTGAGAGTGGCGGCGCATGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAG 2520  
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 Db 2521 CCAAGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
 QY 2581 GGCCTTGAATCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 2640  
 Db 2581 GGCCTTGAATCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGGCT 2640  
 QY 2641 TGTGCTTCAAGTGTGCTGTCTGTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
 Db 2641 TGTGCTTCAAGTGTGCTGTCTGTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
 QY 2701 TTTTAACTTCAAGTGTGCTGTCTGTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
 Db 2701 TTTTAACTTCAAGTGTGCTGTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
 QY 2761 CCCTGCGAGAGAGAGGCTTTTGCAGAGAGCAGACAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
 Db 2761 CCCTGCGAGAGAGAGGCTTTTGCAGAGAGCAGACAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
 QY 2821 CG 2822  
 Db 2821 CG 2822

RESULT 5  
 AAX25359  
 ID AAX25359 standard, cDNA; 2834 BP.  
 XX AAX25359;  
 XX  
 AC  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE Human G protein coupled receptor TSR32 cDNA.  
 XX  
 DE TSR32; G protein coupled receptor; thyroid; human; Bardet Biedl syndrome;  
 KM ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 169..2250  
 FT /\*tag= a  
 XX  
 PN W09915551-A1.  
 XX  
 PD 01-APR-1999.  
 XX  
 PF 24-SEP-1998; 98WO-AU000805.  
 XX  
 PR 24-SEP-1997; 97AU-0009386.  
 XX  
 PA (GARV-) GARVAN INST MEDICAL RES.  
 XX  
 PI Herzog H;  
 XX  
 DR WPI; 1999-244386/20.  
 DR P-PSDB; AAY05730.  
 XX  
 FT New G-protein-coupled receptor designated TSR32.

XX Claim 5; 10-11; 23bp; English.

XX This is the nucleotide sequence of an isolated polynucleotide, the coding  
 CC region of which is also claimed, encoding a new human G protein coupled  
 CC receptor, termed TSR32 (see AAY05730), which is a member of the secretin  
 CC receptor family. TSR32 is expressed in many tissue types, with highest  
 CC expression in the thyroid gland, suggesting that TSR32 has important  
 CC functions in metabolic regulation throughout the body via the thyroid  
 CC gland. TSR32 cDNA was isolated from a human heart cDNA library using a  
 CC 456 bp fragment that had itself identified using degenerate  
 CC oligonucleotides based on conserved regions of the human glucagon-like  
 CC peptide receptor family. The invention provides TSR32 polypeptides,  
 CC polynucleotides, a vector, host cells, an antibody and a non-human  
 CC transgenic animal, as well as a method for detecting agonists or  
 CC antagonists of TSR32, oligonucleotide or polynucleotide probes, an  
 CC antisense polynucleotide, and a method of producing TSR32 or its agonists  
 CC polypeptides by culturing the host cells. The TSR32 protein, its agonists  
 CC and antagonists can be used to regulate thyroid functions in growth,  
 CC development and metabolic activity. The gene for TSR32 has been mapped to  
 CC chromosome 16q31, where Bardet Biedl syndrome, an autosomal recessive  
 CC disorder, has been linked

SQ Sequence 2834 BP; 520 A; 951 C; 767 G; 596 T; 0 U; 0 Other;

Query Match 100.0%; Score 2822; DB 2; Length 2834;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CGGACAGAGGTCCTGCTGTCACACAGGCTGAGTGCAGTGTGATTTGGCTCAT 60  
 Db 7 CGGACAGAGGTCCTGCTGTCACACAGGCTGAGTGCAGTGTGATTTGGCTCAT 66  
 Qy 61 CGTAACTTCAACCTCCCGGGTTCAGTATTCATGCTCAGGCTCCGAGTACTGAG 120  
 Db 67 CGTAACTTCAACCTCCCGGGTTCAGTATTCATGCTCAGGCTCCGAGTACTGAG 126  
 Qy 121 ATTACAGGTGTGATTCACAGAGTGAATCCGTCGAGGAAATGATCTCCCACTGCTG 180  
 Db 127 ATTACAGGTGTGATTCACAGAGTGAATCCGTCGAGGAAATGATCTCCCACTGCTG 186  
 Qy 181 CTGACAGACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 Db 187 CTGACAGACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246  
 Qy 241 GGCCACAGGGAAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
 Db 247 GGCCACAGGGAAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306  
 Qy 301 CACTACAAACCCACACACAGACCTGCGATCTTCATGAGAACTCCGAAAGAGGCTTCA 360  
 Db 307 CACTACAAACCCACACACAGACCTGCGATCTTCATGAGAACTCCGAAAGAGGCTTCA 366  
 Qy 361 GTCCATGCCCCCTTTCCTGACAGCCCACTGCTTCCGATCCCTGACCCCGAGGAGC 420  
 Db 367 GTCCATGCCCCCTTTCCTGACAGCCCACTGCTTCCGATCCCTGACCCCGAGGAGC 426  
 Qy 421 CTACACACTTCTGCTCTACTGAGAACGACATGCTGGAGATTACATCTTCTATGAGC 480  
 Db 427 CTACACACTTCTGCTCTACTGAGAACGACATGCTGGAGATTACATCTTCTATGAGC 486  
 Qy 481 AAGCGTGACTTCTGCTGAGTGAACAAGCTTACGCTTCTGCTTCCAGACCAAGAG 540  
 Db 487 AAGCGTGACTTCTGCTGAGTGAACAAGCTTACGCTTCTGCTTCCAGACCAAGAG 546  
 Qy 541 GAGAGCCTGGCTCAGAGGCCCCCGGCTGTAGCCACTTGTCACTCTGAGTGAAGCCT 600  
 Db 547 GAGAGCCTGGCTCAGAGGCCCCCGGCTGTAGCCACTTGTCACTCTGAGTGAAGCCT 606  
 Qy 601 CAGAACATCAGCTGCGCAGTGCAGCAGCTTCACTTCTCTTCCACAGTCTCTCCAC 660  
 Db 607 CAGAACATCAGCTGCGCAGTGCAGCAGCTTCACTTCTCTTCCACAGTCTCTCCAC 666

Qy 661 AGCGCCGCTCAATGAGCTTCGCTGAGACATGTGCGACCTCAAAAGGAGACCTCAGCTGCTC 720  
 Db 667 AGCGCCGCTCAATGAGCTTCGCTGAGACATGTGCGACCTCAAAAGGAGACCTCAGCTGCTC 726  
 Qy 721 AGCGAGTTCCTGAAGATCCCGAAGAGCCTCAAGAGGCTTCGCTGCTGCTGCTGCTGCTGCTG 780  
 Db 727 AGCGAGTTCCTGAAGATCCCGAAGAGCCTCAAGAGGCTTCGCTGCTGCTGCTGCTGCTGCTG 786  
 Qy 781 CAGCAGTTCGAGAGCCTGAGTGAATCTGACCTCTGTGATTCATGTGGGGCAATGAGT 840  
 Db 787 CAGCAGTTCGAGAGCCTGAGTGAATCTGACCTCTGTGATTCATGTGGGGCAATGAGT 846  
 Qy 841 TCCCTGAGAGAGACCGGATCAACGACAGGTATGAAAGCTCCAGCCACAGCGGCTC 900  
 Db 847 TCCCTGAGAGAGACCGGATCAACGACAGGTATGAAAGCTCCAGCCACAGCGGCTC 906  
 Qy 901 CAGGACCTGACATTCATCCCTCCGACAGAGAGAGAGAGAGAGAGATCATGAGTACTCG 960  
 Db 907 CAGGACCTGACATTCATCCCTCCGACAGAGAGAGAGAGAGAGAGATCATGAGTACTCG 966  
 Qy 961 GTGCTGCTGCTGAGACATCTTTCAGAGAGACCAAAAGCCGAGAGGAGGCTGAGAG 1020  
 Db 967 GTGCTGCTGCTGAGACATCTTTCAGAGAGACCAAAAGCCGAGAGGAGGCTGAGAG 1026  
 Qy 1021 AGACTCCTCCGCTGAGACTTCAGAGCCAAAGCCTGTTCCAGAGCAAGAATTCCAGCCAA 1080  
 Db 1027 AGACTCCTCCGCTGAGACTTCAGAGCCAAAGCCTGTTCCAGAGCAAGAATTCCAGCCAA 1086  
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 Qy 1741 CCATCTTCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800



CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularization syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a nucleic acid sequence of the invention.

XX Sequence 2821 BP, 516 A; 948 C; 765 G; 592 T; 0 U; 0 Other;

Query Match 99.9%; Score 2820; DB 11; Length 2821;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 544 GCCACAGGAGAGACTTTCGCTTGTGACGAGGAGAGAGAGAGAGAGAGAGAGAGAGCTTC 603  
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KW secreted protein; transmembrane protein; ss.  
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1804 GCTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 1863
1855 GCTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 1914
1864 CTGTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 1923
1915 CTGTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 1974
1924 ATGTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 1983
1975 ATGTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2034
1984 CATGTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2043
2035 CATGTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2094
2044 TTCTCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2103
2095 TTCTCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2154
2104 TTCTCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2163
2155 TTCTCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2214
2164 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2223
2215 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2274
2224 ACCTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2283
2275 ACCTGTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2334
2284 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2343
2335 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2394
2344 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2403
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2455 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2512
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2524 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2582
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2633 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2692
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2693 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2752
2703 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2762
2753 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2812
2763 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2821
2813 GGGCCCTGATGATGACGCTGAGTGGCCCTGATGATGAGCAATATGCCCCATCATCTTG 2871

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RESULT 9
AAC78580
ID AAC78580 standard; cDNA; 3819 BP.
XX
AC AAC78580;
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DT 08-FEB-2001 (first entry)
XX
DE Human PRO1083 (UNQ540) nucleotide sequence SEQ ID NO:482.
XX
KM Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens;
XX
PN M0200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000MO-US004341.
XX
PR 08-MAR-1999; 99MO-US005028.
XX PR 12-MAR-1999; 99US-0123957P.
XX PR 29-MAR-1999; 99US-0126773P.
XX PR 21-APR-1999; 99US-0130232P.
XX PR 28-APR-1999; 99US-0131445P.
XX PR 14-MAY-1999; 99US-0134287P.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 30-NOV-1999; 99MO-US028313.
XX PR 02-DEC-1999; 99MO-US028551.
XX PR 02-DEC-1999; 99MO-US028565.
XX PR 16-DEC-1999; 99MO-US030095.
XX PR 30-DEC-1999; 99MO-US031243.
XX PR 30-DEC-1999; 99MO-US031274.
XX PR 05-JAN-2000; 2000MO-US000219.
XX PR 06-JAN-2000; 2000MO-US000277.
XX PR 06-JAN-2000; 2000MO-US000376.
XX
PA (GENT 1) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers LJ, Eaton DL;
PI Ferrara N, Fillardoff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Godowski P, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavlin IU, Kuo SS, Napier MA, Pan J, Piont NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
XX
PT P-PDB; AAB44321.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
XX target bioactive molecules to specific cells, and to modulate cellular
XX activities.
XX
PS Claim 2; Fig 203; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
XX tag) sequences which encode secreted or transmembrane PRO polypeptides.
XX The PRO polynucleotides and polypeptides have cytosolic activity. The
XX polynucleotides and polypeptides can be used for detecting the presence
XX of PRO polypeptides in samples, for linking bioactive molecules to cells
XX and for modulating biological activities of cells, using the polypeptides
XX for specific targeting. The polypeptide targeting can be used to kill the
XX target cells, e.g. for the treatment of cancers. The polypeptide pairs
XX provide specific targeting of bioactive molecules to cells. AAC78600 to
XX AAC78987 represent PCR primers and probes used in the isolation of the
XX PRO polynucleotide sequences
XX
SQ Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;
Query Match 98.6%; Score 2763.4; DB 3; Length 3819;

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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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OY 4 CAGAGGGGTCTCGCTGTGTCA CAGAGGTGAGTCA GTGTGTGTATCTTGGCTCATCTGT 63
Db 55 CTGAGGGGTCTCGCTGTGTCA CAGAGGTGAGTCA GTGTGTGTATCTTGGCTCATCTGT 114
OY 64 AACTTCACTTCCCGGGTTCAAGTATCTATGCTTCAAGCTTCCCGAGTAGTGGATT 123
Db 115 AACTTCACTTCCCGGGTTCAAGTATCTATGCTTCAAGCTTCCCGAGTAGTGGATT 174
OY 124 ACAAGTGTGACTTCAAGAGTGA CTCCGTGAGAGAAATGACTCCCACTGCTGTG 183
Db 175 ACAAGTGTGACTTCAAGAGTGA CTCCGTGAGAGAAATGACTCCCACTGCTGTG 234
OY 184 CAGACGACACTGTTCTGTGAGTCTGTTCTCTGTGTCAAGGTGCCAGGGGGG 243
Db 235 CAGACGACACTGTTCTGTGAGTCTGTTCTCTGTGTCAAGGTGCCAGGGGGG 294
OY 244 CACAGGGAAGCTTCCGTTCTGAGCCAGGGGAA CAGACACACAGGAGAGCTTCAC 303
Db 295 CACAGGGAAGCTTCCGTTCTGAGCCAGGGGAA CAGACACACAGGAGAGCTTCAC 354
OY 304 TACAAACCCACACAGACCTGCGCATCTCA TCGAAGAACTCGAAGAGGCTTCACATC 363
Db 355 TACAAACCCACACAGACCTGCGCATCTCA TCGAAGAGGCTTCACATCAGATC 414
OY 364 CATGCCCCCTTCCCTGTGAGCCCACTGTCTTCCCACTCTTCCCTGACCCAGGGGCTTC 423
Db 415 CATGCCCCCTTCCCTGTGAGCCCACTGTCTTCCCACTCTTCCCTGAGCCAGGGGCTTC 474
OY 424 TACCACTTCTGCTCTATGGAACGACATGCTGAGGAGTTACATCTTCTATGAGCAAG 483
Db 475 TACCACTTCTGCTCTATGGAACGACATGCTGAGGAGTTACATCTTCTATGAGCAAG 534
OY 484 CGTGACTTCTTGTGAGTGA CAAAGCTCTAGCTCTCTGTGCTTCAGACACAGAGAGAG 543
Db 535 CGTGACTTCTTGTGAGTGA CAAAGCTCTAGCTCTCTGTGCTTCAGACACAGAGAGAG 594
OY 544 AGCCGTGCTCAAGGGGCCCCCGCTGTAGCACTTTCGTCA CTTCCGTGAGAGGCTTCAG 603
Db 595 AGCCGTGCTCAAGGGGCCCCCGCTGTAGCACTTTCGTCA CTTCCGTGAGAGGCTTCAG 654
OY 604 AACATCAGAGCTGCGCAGTGCAGCTTCACTTCTCTTCCACAGTCTTCCCA CAG 663
Db 655 AACATCAGAGCTGCGCAGTGCAGCTTCACTTCTCTTCCCA CAGTCTTCCCA CAG 714
OY 664 GCCGCTCACAATGCTCGGTGAGCATGTGCGAGCTCAAAAGGAGCTTCAGAGTCTCAGC 723
Db 715 GCCGCTCACAATGCTCGGTGAGCATGTGCGAGCTCAAAAGGAGCTTCAGAGTCTCAGC 774
OY 724 CAGTTCCTGAAGCATCCCGAAGGCTCAAGAGGAGCTTCAGAGCTCCCGCCGACAGCAG 783
Db 775 CAGTTCCTGAAGCATCCCGAAGGCTCAAGAGGAGCTTCAGAGCTCCCGCCGACAGCAG 834
OY 784 CAGTTGACAGAGCTGAGAGTGA AACTGA CTTCTGTGAGATTCA TGGGGGACATGTGTTC 843
Db 835 CAGTTGACAGAGCTGAGAGTGA AACTGA CTTCTGTGAGATTCA TGGGGGACATGTGTTC 894
OY 844 TTGAGAGAGAGCCGATCAACGCCACAGGTATGGAACCTCAAGCCCA CAGCCGGCTTCAG 903
Db 895 TTGAGAGAGAGCCGATCAACGCCACAGGTATGGAACCTCAAGCCCA CAGCCGGCTTCAG 954
OY 904 GACCTGCACTCACTCCGCGCAGAGAGAGCAGAGCAGAGTCA TGAAGTACTCGTGC 963
Db 955 GACCTGCACTCACTCCGCGCAGAGAGAGCAGAGCAGAGTCA TGAAGTACTCGTGC 1014
OY 964 CTGCTGCTTGAACA CTCTTCCAGAGAGCA AAGCCGCGAGCCGGGAGGCTTGAAGAGAG 1023
Db 1015 CTGCTGCTTGAACA CTCTTCCAGAGAGCA AAGCCGCGAGCCGGGAGGCTTGAAGAGAG 1074
OY 1024 CTCCTCTGTGAGCTTCA GACAGC CCAAGCCCTGTCTCA GAGACA AATTCAGCCAGTCT 1083
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Db 1075 CTCCTCTGTGAGCTTCA GACAGC CCAAGCCCTGTCTCA GAGACA AAGATTCAGCCAGTCT 1134
OY 1084 CTGAGTGAAGAGCTCTTGGGAGTTGTGTACAGAA CACCAAGTAGCCACCTCACAGAG 1143
Db 1135 CTGAGTGAAGAGCTCTTGGGAGTTGTGTACAGAA CACCAAGTAGCCACCTCACAGAG 1194
OY 1144 CCGGTGTGCTCACTTTCAGACACCACTACAGCCGAAAGATGGAACCTTCAATGTGTG 1203
Db 1195 CCGGTGTGCTCACTTTCAGACACCACTACAGCCGAAAGATGGAACCTTCAATGTGTG 1254
OY 1204 TTCTGGGTGAAGACCCCACTTGAAGAGCCCGGGAGCTTGAAGAGTGTGTGAG 1263
Db 1255 TTCTGGGTGAAGACCCCACTTGAAGAGCCCGGGAGCTTGAAGAGTGTGTGAG 1314
OY 1264 ACCGTGAGAGAGAA CCAACAATCTGTCTTGTGAACCACTTGAACCTTGTGAAGT 1323
Db 1315 ACCGTGAGAGAGAA CCAACAATCTGTCTTGTGAACCACTTGAACCTTGTGAAGT 1374
OY 1324 CTGATGTCTCTGAGTGAAGTGAAGCCGCTGACAGAGCTACCTGAGCTCTCTTC 1383
Db 1375 CTGATGTCTCTGAGTGAAGTGAAGCCGCTGACAGAGCTACCTGAGCTCTCTTC 1434
OY 1384 TACGTGGCTGTGTGTCTGTGCTGAGCTGTGCTGTGTCA CCAATTCGCTTACTCTTC 1443
Db 1435 TACGTGGCTGTGTGTCTGTGCTGAGCTGTGCTGTGTCA CCAATTCGCTTACTCTTC 1494
OY 1444 TCCAGAGTCCCTGCTGAGAGAGAACTCGGGAGCTACACATAGAGTGA CAGT 1503
Db 1495 TCCAGAGTCCCTGCTGAGAGAGAACTCGGGAGCTACACATAGAGTGA CAGT 1554
OY 1504 AACCTGTGCTGAGGCTGTCTGCTGAGACAGAGCTTCTGTGAGCAGAGCCGTGAGCC 1563
Db 1555 AACCTGTGCTGAGGCTGTCTGCTGAGACAGAGCTTCTGTGAGCAGAGCCGTGAGCC 1614
OY 1564 CTGAGAGCTGTGAGGCTGTGCTGAGCAGAGCTGTGAGTCTGTGAGCTTCTGTGCTTC 1623
Db 1615 CTGAGAGCTGTGAGGCTGTGCTGAGCAGAGCTGTGAGTCTGTGAGCTTCTGTGCTTC 1674
OY 1624 ACCCTGCTTCTGTGAGTGAAGGCTTCAGAGGAGTCAACCTCTACAGAGCTGTGAGAGTCT 1683
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Db 1735 TTGAGACCTATGTCCTGAGTGAAGGCTTCAGAGGAGTCAACCTCTACAGAGCTGTGAGAGTCT 1794
OY 1744 ATCTTCTGTGAGCAGTGTGAGCCCTGTGAGTGAAGTGAACCTATATGAGCCCATCATCTTG 1803
Db 1795 ATCTTCTGTGAGCAGTGTGAGCCCTGTGAGTGAAGTGAACCTATATGAGCCCATCATCTTG 1854
OY 1804 GCTGTGATAGAGCTTCCAGAGGAGCTCACTACCTTCATGAGTGTGAGTCCGAGACTCC 1863
Db 1855 GCTGTGATAGAGCTTCCAGAGGAGCTCACTACCTTCATGAGTGTGAGTCCGAGACTCC 1914
OY 1864 CTGAGTGAACATCA CCAAGCTGTCTTCAAGCTGTGATTTCTGTTCACATGAGCC 1923
Db 1915 CTGAGTGAACATCA CCAAGCTGTGATTTCTGTTCACATGAGCC 1974
OY 1924 ATGCTAGCA CCAATGAGTGTGAGATCTGTGAGGCTGAGCCCA CCAAGAGTGTCA 1983
Db 1975 ATGCTAGCA CCAATGAGTGTGAGATCTGTGAGGCTGAGCCCA CCAAGAGTGTCA 2034
OY 1984 CAGTGTGATCA CAGTGTGAGGCTCAGAGTGTGCTTGTGAGCTGTGAGGCTGTGATTTTC 2043
Db 2035 CAGTGTGATCA CAGTGTGAGGCTCAGAGTGTGCTTGTGAGCTGTGAGGCTGTGATTTTC 2094
OY 2044 TTCTCTTGTGCTTGTGACCTTCCAGCTTGTGTCTTCACTTTCACATATATACCC 2103
Db 2095 TTCTCTTGTGCTTGTGACCTTCCAGCTTGTGTCTTCACTTTCACATATATACCC 2154
OY 2104 TCTTTCAGAGCTTCTCATCTGATGTAAGTGTGAGTGTGAGGCTGTGAGGCTGTGAGGCT 2163
Db 2155 TCTTTCAGAGCTTCTCATCTGATGTAAGTGTGAGTGTGAGGCTGTGAGGCTGTGAGGCT 2214
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QY 2164 GGGCCCTCCCTCGAAGAGCACTCAGATGGCCGAGGCTCCCATGAGTCCGGGAGC 2223
DB 2215 GGGCCCTCCCTCGAAGAGCACTCAGACAGCGGCGAGGCTCCCATGAGTCCGGGAGC 2274
QY 2224 ACCTGCTCAGCCGCGATCTAGGCTTCAGCCCACTGCTCATGTATGAAGAGAGATGC 2283
DB 2275 ACCTGCTCAGCCGCGATCTAGGCTTCAGCCCACTGCTCATGTATGAAGAGAGATGC 2334
QY 2284 GGGCTTCGTCGACACTGCTGCTGGGCCCCGAGCCAGGCGCCAGGCCAGGAGTACGCG 2343
DB 2335 GGGCTTCGTCGACACTGCTGCTGGGCCCCGAGCCAGGCGCCAGGCCAGGAGTACGCG 2394
QY 2344 CAGACTTTGAAAGCCCAACGACATGAGAGATGGGCGCTTGGCCATGATGATGAGTGC 2403
DB 2395 CAGACTTTGAAAGCCCAACGACATGAGAGATGGGCGCTTGGCCATGATGATGAGTGC 2454
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DB 2455 CCGGGGCTTTTGAATTGGCTTGGGAGCTACTGCGCTCATCTCAGTCCCAAG 2512
QY 2464 GAGCTCAGAGTGGCGCGCATGCTGCTAGGGTACTGATCCCATCTGCTCCCAAGCA 2523
DB 2513 GAGCTCAGAGTGGCGCGCATGCTGCTAGGGTACTGATCCCATCTGCTCCCAAGCA 2572
QY 2524 GCTGGAGGCTGCTGCTCTCTTACAACCCCTGGGCGCAG-CCTCATGCTGGGCGCAG 2582
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QY 2583 CTTTGAATCTTGAAGGCTCTGGGACATCTTAACTCTGAGCCCTGCTGGGACAAATG 2642
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QY 2703 TTAACCTCAGGTGGACCCAGGCGGCAATGGGCGCAGAGGAGACCTTCAAGGCGCAG 2762
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QY 2763 CTGGCGGAGGAGGCGCTTGGCGAGGAGCAGAGAGCGCTGCGCTACTGAGGCC 2821
DB 2813 CTGGCGGAGGAGGCGCTTGGCGAGGAGCAGAGAGCGCTGCGCTACTGAGGCC 2871

RESULT 10
AAS21446
ID AAS21446 standard; cDNA; 3819 BP.
XX AAS21446;
AC
XX
XX 24-OCT-2001 (first entry)
DT
XX
XX Human cDNA sequence encoding for PRO1083 polypeptide.
DE
XX
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KM prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KM ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX A-peptide; factor VIIA; gene therapy; ss.
OS Homo sapiens.
XX
XX WO200140466-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 01-DEC-2000; 2000WO-US032678.
PF
XX
XX 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.

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PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

(GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z,
XX WPI: 2001-408281/43.
XX P-PSDB; AMU12374.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
XX other PRO polypeptides, link bioactive molecules to cells expressing PRO
XX polypeptides, and detect the presence of mammalian tumors e.g. lung,
XX breast, prostate, cervical.
XX
XX Claim 3; Fig 405; 813pp; English.
XX
XX AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
XX polypeptides. The PRO polypeptides are useful to detect other PRO
XX polypeptides, to link bioactive molecules to cells expressing PRO
XX polypeptides, to modulate biological activities of cells expressing PRO
XX polypeptides, and to detect the presence of mammalian lung, colon,
XX breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX polypeptide expression in a cell sample to that in a control sample. Some
XX of the 275 sequences are also useful to stimulate the release of tumour
XX necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
XX differentiation of chondrocytes, the proliferation or gene expression in
XX pericyte cells, the release of proteoglycans from cartilage, the
XX proliferation of inner ear utricular supporting cells or of T-
XX lymphocytes, the release of a cytokine from peripheral blood monocytes
XX (PBMCs), or the proliferation of endothelial cells. Some of the PRO
XX polypeptides may modulate glucose or free fatty acid uptake by skeletal
XX muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
XX VIIA. The PRO polypeptides can be used in assays to identify molecules
XX involved in binding interactions. The polynucleotides encoding PRO
XX polypeptides can be used to generate probes, antisense RNA/DNA,
XX transgenic or knock out animals and can be used in gene therapy
XX

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Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;  
Query Match 98.6%; Score 2783.4; DB 4; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
4 CAGCAGGGTCTGCTCTGTGACACAGGCTGAGTGTGATGATCTTGGCTCATGCT 63  
Db CTGAGGGGTCTGCTCTGTGACACAGGCTGAGTGTGATGATCTTGGCTCATGCT 114  
Qy 64 AACCTCACTCCGGGTTCAAGTATTCATGCTCTACGCTCCAGTGTGGATT 123  
Db 115 AACCTCACTCCGGGTTCAAGTATTCATGCTCTACGCTCCAGTGTGGATT 174  
Qy 124 ACAGTGTGATCTTCCAGAGTGACTCCGTGGAGGAATGATCTCCCACTGCTGTG 183  
Db 175 ACAGTGTGATCTTCCAGAGTGACTCCGTGGAGGAATGATCTCCCACTGCTGTG 234  
Qy 184 CAGACGACATGTTCTGCTGAGTGTGCTCTTCTGTCAGAGTGTCCACGGCAGGGGC 243  
Db 235 CAGACGACATGTTCTGCTGAGTGTGCTCTTCTGTCAGAGTGTCCACGGCAGGGGC 294  
Qy 244 CACAGGGAAGATTTGCTTGTGACGCGACGCGAAACAGACACAGAGACGCTCCAC 303  
Db 295 CACAGGGAAGATTTGCTTGTGACGCGACGCGAAACAGACACAGAGACGCTCCAC 354  
Qy 304 TACAAACCCACACGACCTGTGGCATCTCCATCGGAATCTCCGAGAGGGCCCTCAAGTC 363  
Db 355 TACAAACCCACACGACCTGTGGCATCTCCATCGGAATCTCCGAGAGGGCCCTCAAGTC 414  
Qy 364 CATGGCCCTTTCCTGACAGCCCACTGCTTCCGATCTTCCCTGACCCAGGGGCTTC 423  
Db 415 CATGGCCCTTTCCTGACAGCCCACTGCTTCCGATCTTCCCTGACCCAGGGGCTTC 474  
Qy 424 TACCACTTCTGCTCTACTGAAACGACATGCTGGAGATTCATTTCTTATGGCAAG 483  
Db 475 TACCACTTCTGCTCTACTGAAACGACATGCTGGAGATTCATTTCTTATGGCAAG 534  
Qy 484 CGTGACTTCTGCTGAGTGAACAAGCTCTAGCTCTGCTGCTCCAGACAGAGAGAG 543  
Db 535 CGTGACTTCTGCTGAGTGAACAAGCTCTAGCTCTGCTGCTCCAGACAGAGAGAG 594  
Qy 544 AGCTGTGCTCAGGGCCCGCTGTATGACACTTCTGTGACCTCTGTGTGAGCCCTCAG 603  
Db 595 AGCTGTGCTCAGGGCCCGCTGTATGACACTTCTGTGACCTCTGTGTGAGCCCTCAG 654  
Qy 604 AACATCAAGCTGTGCCAGTGTCCGACGCTTCACTTCTCTTCCACAGTCTCTCCACAG 663  
Db 655 AACATCAAGCTGTGCCAGTGTCCGACGCTTCACTTCTCTTCCACAGTCTCTCCACAG 714  
Qy 664 GCGCTCAAAATGCTCGGTGAGCATGTGGAGCTGAAAAGGAGCTCCAGCTGTCAAG 723  
Db 715 GCGCTCAAAATGCTCGGTGAGCATGTGGAGCTGAAAAGGAGCTCCAGCTGTCAAG 774  
Qy 724 CAGTTCCTGAAGCATCCCAAGAGGCTCAAGAGGCGCTCGCTGCGCCCGCAGCCAG 783  
Db 775 CAGTTCCTGAAGCATCCCAAGAGGCTCAAGAGGCGCTCGCTGCGCCCGCAGCCAG 834  
Qy 784 CAGTTCAGAGCTGTGAGTGAATCTGTGATGATTCATGGGGGACATGTGTCTC 843  
Db 835 CAGTTCAGAGCTGTGAGTGAATCTGTGATGATTCATGGGGGACATGTGTCTC 894  
Qy 844 TTTCAGAGGAGCGGATCAACGCGCATGTGAAAGTCCAGGCCACAGCGCGCTCAG 903  
Db 895 TTTCAGAGGAGCGGATCAACGCGCATGTGAAAGTCCAGGCCACAGCGCGCTCAG 954  
Qy 904 GACCTGCAATTCACCTCCCGCAGAGAGAGACAGACGATCATGAGTACTGCTG 963  
Db 955 GACCTGCAATTCACCTCCCGCAGAGAGAGACAGACGATCATGAGTACTGCTG 1014  
Qy 964 CTGCTGCTGGAACATCTTTCAGAGAGACGAAAGCGCGAGCGGGAGGCTGAGAGAGA 1023  
Db 1015 CTGCTGCTGGAACATCTTTCAGAGAGACGAAAGCGCGAGCGGGAGGCTGAGAGAGA 1074

Qy 1024 CTCTCTGTGTGACCTTACAGACGCAAGCCCTGTTCAGAGGACAAAGATTCACGCAAGTC 1083  
Db 1075 CTCTCTGTGTGACCTTACAGACGCAAGCCCTGTTCAGAGGACAAAGATTCACGCAAGTC 1134  
Qy 1084 CTGGGTGAGAGGCTTGGGATGTGTACAGAACCAAGATGACCACTTCAAGAG 1143  
Db 1135 CTGGGTGAGAGGCTTGGGATGTGTGTACAGAACCAAGATGACCACTTCAAGAG 1194  
Qy 1144 CCGGTGTGCTCACTTTCAGACACGCTACAGCGGAAATGTGATCTGTCAATGTGTG 1203  
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Db 1255 TTCTGGGTGAAAGCCCACTTGAAGACCCCGGGGCAATTGAGAGTGTGGGTGTAG 1314  
Qy 1264 ACCGTGAGAGAGAAACCAAACTCTGCTTGTGCAACACTTGAACCTTACCTTGTGAGT 1323  
Db 1315 ACCGTGAGAGAGAAACCAAACTCTGCTTGTGCAACACTTGAACCTTACCTTGTGAGT 1374  
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Db 1375 CTGATGTCTCTGTGTGAGAGTGTGACGCGGTGACAGACACTACCTGAGCTCTTCC 1434  
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Db 1435 TACGTGGCTGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494  
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Db 1495 TCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1554  
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Db 1615 CTGACAGCTGTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1674  
Qy 1624 ACCGTGCTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683  
Db 1675 ACCGTGCTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1734  
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Db 1735 TTTGGCACTATGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1794  
Qy 1744 ATCTTTCTGTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1803  
Db 1795 ATCTTTCTGTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1854  
Qy 1804 GCTGTGATGAGACTCAAGAGGCGTCAATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1863  
Db 1855 GCTGTGATGAGACTCAAGAGGCGTCAATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1914  
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Qy 1924 ATGTGACCAACATGTGTGTGAGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1983  
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QY 2224 ACCCTGCGGCGGCTGAGAGCACTGAGCTGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 2283
DB 2275 ACCCTGCGGCGGCTGAGAGCACTGAGCTGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 2334
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DB 2813 CTGCGGAGAGGCGGCTGAGAGGCGGCTGAGAGGCGGCTGAGAGGCGGCTGAGAGGCGGCTGAGAGGCGGCT 2871

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## RESULT 11

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ABK3602
ID ABRK3602 standard; cDNA; 3819 BP.
XX
AC ABRK3602;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 133.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.

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PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 25-JUL-2000; 2000US-0220693P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006666.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
XX PT Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX PI WPI: 2002-1172001/22.
XX DR P-PSDB: MAU083658.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX PT useful for treating a PRO related disorder and for diagnosing tumors such
XX PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
XX PT or liver tumor.
XX
XX Claim 2; Fig 133; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX CC agonists and antagonists are useful for treating a PRO related disorder.
XX CC The PRO polypeptides are useful for diagnosing tumors, especially lung
XX CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
XX CC liver tumor. The PRO polypeptides are useful for stimulating the
XX CC proliferation of, or gene expression, in pericyte cells, for stimulating
XX CC the proliferation or differentiation of chondrocyte cells, for
XX CC stimulating the release of tumour necrosis factor-alpha from human blood,
XX CC for stimulating or inhibiting the proliferation of normal human dermal
XX CC fibroblast cells. The PRO polypeptide may also be used as molecular
XX CC weight markers and for tissue typing. The PRO nucleic acids have
XX CC applications in molecular biology, including use as hybridisation probes,
XX CC and in chromosome and gene mapping. ABRK3536-ABK3657 represent human PRO
XX CC protein coding sequences of the invention
XX
XX Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;
SQ

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Query Match 98.6%; Score 2783.4; DB 6; Length 3819;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2810; Conservative 6; Indels 3; Gaps 2;

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QY 64 AACCTCCAGCTCCCGGGTTCAGAGTATCTCACTGCTCAGCTCCCGAGTACCTGGGATT 123
DB 115 AACCTCCAGCTCCCGGGTTCAGAGTATCTCACTGCTCAGCTCCCGAGTACCTGGGATT 174
QY 124 ACAGGTGTGACTTCCAGAGTATCTGCTGAGAGGCGGCTGAGAGGCGGCTGAGAGGCGGCTGAGAGGCGGCT 183

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Db 235 CAGACGACATGTTCTGCTGAGTGTCTCTTCTGCTGCTCAAGGTCCTCCAGGGAGG 294  
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Db 415 CATGCCCCCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 474  
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Qy 604 AACATCAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663  
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Qy 1864 CTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1923  
Db 1915 CTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1974  
Qy 1924 ATGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1983  
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Db 2395 CAGACTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2454

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QY 2404 CCGGCGCTGGGCTTTTGAATTTGGCTTTGGGAGCACTGCGCTCTCACTCACTCCACG 2463
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DB 2455 CCGGG--CTGGGCTTTTGAATTTGGCTTTGGGAGCACTGCGCTCTCACTCACTCCACG 2512
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QY 2464 GGACTCAGAGTGGCGCGCATGCTGCTAGGGTACTGATCCCACTGCTCCAAACCA 2523
    |||||
DB 2513 GGACTCAGAGTGGCGCGCATGCTGCTAGGGTACTGATCCCACTGCTCCAAACCA 2572
    |||||
QY 2524 GCTGAGAGCTGCTGCTCTCTTACAACTCTGGGCGCAG--CCTCATGCTGGGGCGCAGG 2582
    |||||
DB 2573 GCTGAGAGCTGCTGCTCTCTTACAACTCTGGGCGCAG--CCTCATGCTGGGGCGCAGG 2632
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QY 2583 CCTTGATCTTGAAGGCTGTCGACATCTTATCTGTGCCCCCTGCTGGGAGCAAAATG 2642
    |||||
DB 2633 CCTTGATCTTGAAGGCTGTCGACATCTTATCTGTGCCCCCTGCTGGGAGCAAAATG 2692
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QY 2763 CTGGCGAGAGAGAGGCGCTTTGGCCAGAGCAGACAGAGAGCTCGGCTACCTGAGAGCC 2821
    |||||
DB 2813 CTGGCGAGAGAGAGGCGCTTTGGCCAGAGCAGACAGAGAGCTCGGCTACCTGAGAGCC 2871
    |||||

```

## RESULT 13

ABL95606 standard; cDNA; 3819 BP.

19-JUL-2002 (first entry)

Human angiogenesis related cDNA PRO1083 SEQ ID NO: 91.

Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiac; cystostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.

Homo sapiens.

WO200208284-A2.

31-JAN-2002.

09-JUL-2001; 2001WO-US021735.

20-JUL-2000; 2000US-0219556P.

25-JUL-2000; 2000US-0220624P.

28-JUL-2000; 2000WO-US020710.

02-AUG-2000; 2000US-022695P.

17-AUG-2000; 2000US-0264365P.

23-AUG-2000; 2000WO-US023522.

07-SEP-2000; 2000US-0230978P.

18-SEP-2000; 2000US-00664610.

24-OCT-2000; 2000US-0242922P.

08-NOV-2000; 2000US-0070923P.

08-NOV-2000; 2000WO-US030952.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-0074725P.

22-JAN-2001; 2000WO-US04956P.

28-FEB-2001; 2001US-0076498P.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.

XX (GETH ) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

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PA (GERR) GERRITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GURN) GURNEY A L.

PA (HILL) HILLAN K J.

PA (MARS) MARSTERS S A.

PA (PANU) PAN J.

PA (FRON) FRON N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

DR WPI; 2002-171999/22.

XX P-PSDB; ABB95468.

DR Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;

XX SQ

QY 4 CAGCAGGCTGCTGCTCTGTGTCACACAGGCTGAGTGCAGTGTGATCTTGGCTCATGCT 63

DB 55 CTGAGAGGCTGCTGCTCTGTGTCACACAGGCTGAGTGCAGTGTGATCTTGGCTCATGCT 114

QY 64 AACCTCCACCTCCCGGGTCAAGTATCTCAATGCTCAGCTCCGAGTAGCTGGATT 123

DB 115 AACCTCCACCTCCCGGGTCAAGTATCTCAATGCTCAGCTCCGAGTAGCTGGATT 174

QY 124 ACAGGTGTGACTTCCAGAGTGAATCTCGTCCGAGGAAATGAATCTCCCACTGCTGCTG 183

DB 175 ACAGGTGTGACTTCCAGAGTGAATCTCGTCCGAGGAAATGAATCTCCCACTGCTGCTG 234

QY 184 CAGACGACACTGTCTGCTGAGTCTGCTTCTTCTGCTCAAGGTGCCACGCGCAGGGGC 243

Claim 1; Fig 91; 567bp; English.

The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention

Query Match 98.6%; Score 2783.4; DB 6; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;







XX Ahenkazi AJ, Baker KP, Borestein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Geber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Kijavini J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,  
 PI Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI: 2003-328860/31.  
 DR P-PSDB; AB072273.  
 XX  
 PT New secreted and transmembrane nucleic acids and polypeptides, designated  
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or  
 PT cancer.  
 PS  
 PS Claim 2; Fig 203; 453pp; English.  
 CC  
 CC The invention describes an isolated nucleic acid (1) comprising, or which  
 CC is at least 80 % sequence identity to, or the full-length coding sequence  
 CC of, any of 118 300-2100 nucleotide sequences, which encodes its  
 CC corresponding PRO polypeptide selected from 118 100-700 amino acid  
 CC sequences, all given in the specification. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS, cancer, or diabetic complications. The nucleic  
 CC acids are useful as hybridisation probes, in chromosome and gene mapping,  
 CC and in generating antisense RNA or DNA. The polypeptides are useful as  
 CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful  
 CC in tissue typing. This sequence encodes a novel human secreted and  
 CC transmembrane PRO polypeptide  
 CC  
 XX  
 SQ Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;  
 Query Match 98.6%; Score 2783.4; DB 8; Length 3819;  
 Best Local Similarity 99.7%; Pred. No. 0; Mismatches 6; Indels 3; Gaps 2;  
 Matches 2810; Conservative 0;  
 Oy 4 CAGCAGGCTCTGCTCTGTCACACAGGCTGAGTGTGTGATCTTGGCTCATCT 63  
 Db 55 CTGAGAGGCTCTGCTCTGTCACACAGGCTGAGTGTGTGATCTTGGCTCATCT 114  
 Oy 64 AACCTCCACCTCCCGGCTTCAAGTATTTCTATGCTCTCAGCTCCCGAGTACCTGGATT 123  
 Db 115 AACCTCCACCTCCCGGCTTCAAGTATTTCTATGCTCTCAGCTCCCGAGTACCTGGATT 174  
 Oy 124 ACAGGTGTGATCTTCCAGAGTGAATCCGTCGAGAGGAATGACTCCCAAGTGTGCTG 183  
 Db 175 ACAGGTGTGATCTTCCAGAGTGAATCCGTCGAGAGGAATGACTCCCAAGTGTGCTG 234  
 Oy 184 CAGACGACATGTTCTGCTGATGCTGCTTCTCTGATCCAGAGTCCCAAGGAGGCTC 243  
 Db 235 CAGACGACATGTTCTGCTGATGCTGCTTCTCTGATCCAGAGTCCCAAGGAGGCTC 294  
 Oy 244 CACAGGGAAGATCTTGTCTTGTGCAACCGAGGGAACCAAGACACAGAGGAGGCTCCAC 303  
 Db 295 CACAGGGAAGATCTTGTCTTGTGCAACCGAGGGAACCAAGACACAGAGGAGGCTCCAC 354  
 Oy 304 TACAAACCCACACAGAGCTGAGCTATCTCATGAGAACTCCGAAGAGGCTCTCAAGTC 363  
 Db 355 TACAAACCCACACAGAGCTGAGCTATCTCATGAGAACTCCGAAGAGGCTCTCAAGTC 414  
 Oy 364 CATGCCCTTTCCCTGAGGCAACCTGCTTCCGATCTTCCCTGACCCCAAGGAGGCTC 423  
 Db 415 CATGCCCTTTCCCTGAGGCAACCTGCTTCCGATCTTCCCTGACCCCAAGGAGGCTC 474  
 Oy 424 TACCACTTCTGCTCTCACTGGAACCGACATGCTGGAGGATTAATCTTCTTATGGAAG 483  
 Db 475 TACCACTTCTGCTCTCACTGGAACCGACATGCTGGAGGATTAATCTTCTTATGGAAG 534  
 Oy 484 CGTGACTTCTTGTGATGACCAAGGCTCTAGCTCTCTGCTTCCAGACACAGAGAGAG 543  
 Db 535 CGTGACTTCTTGTGATGACCAAGGCTCTAGCTCTCTGCTTCCAGACACAGAGAGAG 594

Oy 544 AGCTTGCTGAGGAGGCCCCCGCTTTAGCACTTCTGTCACCTCTGAGGAGGCTCAG 603  
 Db 595 AGCTTGCTGAGGAGGCCCCCGCTTTAGCACTTCTGTCACCTCTGAGGAGGCTCAG 654  
 Oy 604 AACATGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663  
 Db 655 AACATGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 714  
 Oy 664 GCGGCTCAAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 723  
 Db 715 GCGGCTCAAAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 774  
 Oy 724 CAGTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 783  
 Db 775 CAGTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 834  
 Oy 784 CAGTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 843  
 Db 835 CAGTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 894  
 Oy 844 TTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 903  
 Db 895 TTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 954  
 Oy 904 GACCTGACATCCACTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 963  
 Db 955 GACCTGACATCCACTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1014  
 Oy 964 CTGCTGCTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1023  
 Db 1015 CTGCTGCTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1074  
 Oy 1024 CTGCTGCTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1083  
 Db 1075 CTGCTGCTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1134  
 Oy 1084 CTGCTGCTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143  
 Db 1135 CTGCTGCTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1194  
 Oy 1144 CCGGTGTGCTCACTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203  
 Db 1195 CCGGTGTGCTCACTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1254  
 Oy 1204 TTCTGTGTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1263  
 Db 1255 TTCTGTGTGAGAACCTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1314  
 Oy 1264 ACCGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1323  
 Db 1315 ACCGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1374  
 Oy 1324 CTGATGTGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1383  
 Db 1375 CTGATGTGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1434  
 Oy 1384 TAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1443  
 Db 1435 TAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1494  
 Oy 1444 TCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1503  
 Db 1495 TCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1554  
 Oy 1504 AACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1563  
 Db 1555 AACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1614  
 Oy 1564 CTGACAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1623  
 Db 1615 CTGACAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1674  
 Oy 1624 ACTGTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1683

1675 ACCTGACCTTCTGGATGGGCTCGAGGGGTACAACCTTACCGACTGTGGTGGAGGCTC 1734  
1684 TTTGGACCTTATGTCCTGGCTGCTACTCAAGGCTGAGCGGCTGGGGCTTCCCC 1743  
1735 TTTGGACCTTATGTCCTGGCTGCTACTCAAGGCTGAGCGGCTGGGGCTTCCCC 1794  
1744 ATCTTCTGTGTGACGCTGTGGCTTGGTGTGATGTGACAACTATGCCCCATCATCTTG 1803  
1795 ATCTTCTGTGTGACGCTGTGGCTTGGTGTGATGTGACAACTATGCCCCATCATCTTG 1854  
1804 GCTGTGTGATGAGATCTCGAGGGGCTCATACCTTCCATGTGTGATCCGGGATCC 1863  
1855 GCTGTGTGATGAGATCTCGAGGGGCTCATACCTTCCATGTGTGATCCGGGATCC 1914  
1864 CTGGTCACTATCATCAACCACTGGGGCTTCACTGCTGTGTGTCTGTCAACATGACC 1923  
1915 CTGGTCACTATCATCAACCACTGGGGCTTCACTGCTGTGTGTCTGTCAACATGACC 1974  
1924 ATGTAGCCACCAATGATGTGTGAGATCTGTGGCTGTGGCCGCCACACCCAAAGTGTCA 1983  
1975 ATGTAGCCACCAATGATGTGTGAGATCTGTGGCTGTGGCCGCCACACCCAAAGTGTCA 2034  
1984 CATGTGTGTGACCTGTGGGCTTCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2043  
2035 CATGTGTGTGACCTGTGGGCTTCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2094  
2044 TTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2103  
2095 TTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2154  
2104 TCTTTCAGAGGCTTCTCATCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2163  
2155 TCTTTCAGAGGCTTCTCATCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2214  
2164 GGGCCCTCCCTCTGAAGGCACTCTGAGCTGGGCGGCTCCCATCAGCTCGGGCAGC 2223  
2215 GGGCCCTCCCTCTGAAGGCACTCTGAGCTGGGCGGCTCCCATCAGCTCGGGCAGC 2274  
2224 ACCTGTCCAGCGGCTTGTGAGCTTCCAGCCCACTGCTCATGTGTGTGTGTGTGTGTGT 2283  
2275 ACCTGTCCAGCGGCTTGTGAGCTTCCAGCCCACTGCTCATGTGTGTGTGTGTGTGTGT 2334  
2284 GGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2343  
2335 GGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2394  
2344 CAGACTTGTGAAAGCCCAAGCACTGAGAGATGTGGCGTGTGTGTGTGTGTGTGTGTGT 2403  
2395 CAGACTTGTGAAAGCCCAAGCACTGAGAGATGTGGCGTGTGTGTGTGTGTGTGTGTGT 2454  
2404 CCGGGGCTGGGCTTGTGAAATGTGGCTTGGGGACTAATCGGCTGTCACTCACTGCCAGC 2463  
2455 CCGGGGCTGGGCTTGTGAAATGTGGCTTGGGGACTAATCGGCTGTCACTCACTGCCAGC 2512  
2464 GGAATCAAGAGTGGCGGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2523  
2513 GGAATCAAGAGTGGCGGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2572  
2524 GCTGAGGCTGGTGTCTCTCTTACAACCTCTGGGCCAGCTCATGTGTGTGTGTGTGTGTGT 2582  
2573 GCTGAGGCTGGTGTCTCTCTTACAACCTCTGGGCCAGCTCATGTGTGTGTGTGTGTGTGT 2632  
2583 CCTTGTGATTTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2642  
2633 CCTTGTGATTTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2692  
2643 TGGCTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2702  
2693 TGGCTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2752  
2703 TTAACCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2762

Db 2753 TTAACCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2812  
Qy 2763 CTGGCGAGAGAGAGGCTTGTGCGAGAGACAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 2821  
Db 2813 CTGGCGAGAGAGAGGCTTGTGCGAGAGACAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 2871  
RESULT 15  
ACN03805  
ID ACN03805 standard; cDNA, 3819 BP.  
XX  
AC ACA03805;  
XX  
DT 23-MAY-2003 (first entry)  
XX  
XX  
DE cDNA encoding human PRO polypeptide #203.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumor necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;  
KW 88.  
OS Homo sapiens.  
XX  
PN US2003036180-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 09-MAY-2002; 2002US-00143114.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 02-DEC-1999; 99WO-US030095.  
PR 16-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.

06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US000355.  
PR 18-FEB-2000; 2000WO-US000431.  
PR 18-FEB-2000; 2000WO-US000434.  
PR 22-FEB-2000; 2000WO-US000441.  
PR 24-FEB-2000; 2000WO-US000491.  
PR 24-FEB-2000; 2000WO-US000504.  
PR 01-MAR-2000; 2000WO-US000561.  
PR 02-MAR-2000; 2000WO-US000574.  
PR 02-MAR-2000; 2000WO-US000584.  
PR 10-MAR-2000; 2000WO-US000639.  
PR 15-MAR-2000; 2000WO-US000684.  
PR 20-MAR-2000; 2000WO-US000737.  
PR 21-MAR-2000; 2000WO-US000843.  
PR 30-MAR-2000; 2000WO-US001370.  
PR 17-MAY-2000; 2000WO-US014042.  
PR 22-MAY-2000; 2000WO-US014941.  
PR 30-MAY-2000; 2000WO-US015264.  
PR 02-JUN-2000; 2000WO-US020710.  
PR 28-JUN-2000; 2000WO-US022031.  
PR 11-AUG-2000; 2000WO-US023522.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023528.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001US-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001WO-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
XX (GSETH ) GENENTECH INC.  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerilisen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;  
XX  
XX WPI: 2003-332040/31.  
DR P-PSDB; ABU66772.  
XX  
XX New secreted and transmembrane PRO nucleic acids, useful for gene  
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue  
PT typing, and in chromosome identification.  
XX  
XX Claim 2; Fig 405; 660pp; English.  
XX  
XX The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for  
CC identifying agonists or antagonists. The PRO polypeptides are useful for  
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from  
CC human blood, for stimulating the proliferation or differentiation of  
CC chondrocytes, and detecting the presence of tumours. The polynucleotide  
CC sequences encoding PRO polypeptides are useful as hybridisation probes,  
CC in chromosome and gene mapping, in the generation of antisense RNA and  
CC DNA, in the preparation of PRO polypeptides, for generating transgenic  
CC animals or knockout animals, for the genetic analysis of individuals with  
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs  
CC encoding the human PRO polypeptides of the invention. Note: The sequence  
CC data for this patent was obtained in electronic format directly from the  
CC USPTO web site at [seqdata.uspto.gov/patidb/identity.html](http://seqdata.uspto.gov/patidb/identity.html)  
XX  
SQ Sequence 3819 BP; 789 A; 1221 C; 996 G; 813 T; 0 U; 0 Other;  
Query Match 98.6%; Score 2783.4; DB 8; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0; Mismatches 6; Indels 3; Gaps 2;  
Matches 2810; Conservative  
QY 4 CAGCAGGCTCTGCTGTCACACAGAGCTGAGTGTGATCTTGGCTCATCGT 63  
DB CTGAGAGGCTCTGCTGTCACACAGAGCTGAGTGTGATCTTGGCTCATCGT 114  
QY AACCTCCACCTCCCGGGTTCAAGTATCTCATGCTTCCGAGTACCTGGATT 123  
DB AACCTCCACCTCCCGGGTTCAAGTATCTCATGCTTCCGAGTACCTGGATT 174  
QY 124 ACAAGTGTGATCTTCCAAAGTATCTTCCGAGTGTGATCTTGGCTCATCGT 183  
DB ACAAGTGTGATCTTCCAAAGTATCTTCCGAGTGTGATCTTGGCTCATCGT 234  
QY 175 ACAAGTGTGATCTTCCAAAGTATCTTCCGAGTGTGATCTTGGCTCATCGT 234  
DB ACAAGTGTGATCTTCCAAAGTATCTTCCGAGTGTGATCTTGGCTCATCGT 294  
QY 235 CAGACGACACTGTTCTGCTGATGTTCTTCTTCCAAAGTGTGATCTTGGCTCATCGT 294  
DB CAGACGACACTGTTCTGCTGATGTTCTTCTTCCAAAGTGTGATCTTGGCTCATCGT 303  
QY 244 CACAGGAGAGACTTCTGCTGATGTTCTTCTTCCAAAGTGTGATCTTGGCTCATCGT 303  
DB CACAGGAGAGACTTCTGCTGATGTTCTTCTTCCAAAGTGTGATCTTGGCTCATCGT 354  
QY 295 CACAGGAGAGACTTCTGCTGATGTTCTTCTTCCAAAGTGTGATCTTGGCTCATCGT 354  
DB CACAGGAGAGACTTCTGCTGATGTTCTTCTTCCAAAGTGTGATCTTGGCTCATCGT 414  
QY 304 TACCAATCCCAACCAAGCTGCGATCTTCCAAAGTGTGATCTTGGCTCATCGT 363  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:22:24 ; Search time 469 Seconds  
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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	554.4	19.6	556	4	US-09-262-537-45 Sequence 45, Appl
3	215	7.6	356	4	US-09-513-999C-12063 Sequence 12063, A
4	205.2	7.3	354	4	US-09-621-976-10391 Sequence 10391, A
5	115.4	4.1	1651	3	US-09-484-970B-17 Sequence 17, Appl
6	111	3.9	3453	4	US-09-949-016-12256 Sequence 12256, A
7	111	3.9	34540	4	US-09-949-016-13156 Sequence 13156, A
8	111	3.9	45546	3	US-09-146-053-6 Sequence 6, Appl
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45	108.6	3.8	86213	4	US-09-949-016-17240 Sequence 17240, A

#### ALIGNMENTS

RESULT 1  
US-09-276-531-78  
Sequence 78, Application US/09276531

Patent No. 6183968

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yee, Henry

APPLICANT: Reddy, Roopa

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING

RECEIPTS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,531

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/079,677

FILING DATE: March 27, 1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lynn E. Murry, Ph.D.

REGISTRATION/DOCKET NUMBER: 42,918

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

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INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 3090 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BRAINOT14



CLONE: 1595762  
US-09-276-531-78

Query Match 73.6%; Score 2075.8; DB 3; Length 3090;  
Beet Local Similarity 99.1%; Pred. No. 0;  
Matches 2139; Conservative 0; Mismatches 14; Indels 6; Gaps 5;

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DB 2075 TGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2134
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QY 2763 CTGGCGGAGAGAGCCCTTTTCCAGAGACACAGAGAGCTGGCTTACTTGAAGCC 2821  
Db 2135 CTGGCGGAGAGAGCCCTTTTCCAGAGACACAGAGAGCTGGCTTACTTGAAGCC 2193

RESULT 2  
US-09-262-537-45  
; Sequence 45, Application US/09262537  
; Patent No. 6479256  
; GENERAL INFORMATION:  
; APPLICANT: Hayflick, Joel  
; TITLE OF INVENTION: Lectomedin Materials and Methods  
; FILE REFERENCE: 2786/35307  
; CURRENT APPLICATION NUMBER: US/09/262,537  
; CURRENT FILING DATE: 1999-03-04  
; EARLIER APPLICATION NUMBER: 60/076,782  
; EARLIER FILING DATE: 1998-03-04  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 45  
; LENGTH: 556  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-262-537-45

Query Match 19.6%; Score 554.4; DB 4; Length 556;  
Best Local Similarity 99.8%; Pred. No. 6,7e-118;  
Matches 555; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1579 GCTGGCTGCGGAGGAGTGCATCTTCTGCACTTCTCCCTGCTCACTGCTCTTCTG 1638  
Db 1 GCTGGCTGCGGAGGAGTGCATCTTCTGCACTTCTCCCTGCTCACTGCTCTTCTG 60  
QY 1639 ATGGGCTTGAAGGGGTACAACTTACCGGATCTGCTGCTGAGGCTTTTGGACCTATGTC 1698  
Db 61 ATGGGCTTGAAGGGGTACAACTTACCGGATCTGCTGCTGAGGCTTTTGGACCTATGTC 120  
QY 1699 CTGGCTTACTTCAAGCTGAGCGGCGCATGGGGCTGGGGCTCCCATCTTTCTGAGAG 1758  
Db 121 CTGGCTTACTTCAAGCTGAGCGGCGCATGGGGCTGGGGCTCCCATCTTTCTGAGAG 180  
QY 1759 CTGGTGGCCCTGATGATGAGCACTATGAGCCCATCATCTTGGCTGATGAGACT 1818  
Db 181 CTGGTGGCCCTGATGATGAGCACTATGAGCCCATCATCTTGGCTGATGAGACT 240  
QY 1819 CCAAGAGGGGCTCATCTACCTTCTCATGCTGATCGGAGCTCCCTGCTCACTATC 1878  
Db 241 CCAAGAGGGGCTCATCTACCTTCTCATGCTGATCGGAGCTCCCTGCTCACTATC 300  
QY 1879 ACCAAGCTGGGCTCTTCAAGCGCTGCTTCTGTTCAACATGGCCATGAGCCACATG 1938  
Db 301 ACCAAGCTGGGCTCTTCAAGCGCTGCTTCTGTTCAACATGGCCATGAGCCACATG 360  
QY 1939 GTGGTGCAGATCTTGGCGGTGCGCCCAACACCAAAAGTGTCAATGCTGACACTG 1998  
Db 361 GTGGTGCAGATCTTGGCGGTGCGCCCAACACCAAAAGTGTCAATGCTGACACTG 420  
QY 1999 CTGGGCTTCAAGCTGCTTCTGAGCTGCGCTGGGCTGATCTTCTTCTCTTCTGCTTC 2058  
Db 421 CTGGGCTTCAAGCTGCTTCTGAGCTGCGCTGGGCTGATCTTCTTCTCTTCTGCTTC 480  
QY 2059 GGCACCTTCAAGCTTGTGCTCTTCACTTTTCAAGCATCACTCTTCAAGGCTTC 2118  
Db 481 GGCACCTTCAAGCTTGTGCTCTTCACTTTTCAAGCATCACTCTTCAAGGCTTC 540  
QY 2119 CTCATCTTCACTGCTT 2134  
Db 541 CTCATCTTCACTGCTT 556

RESULT 3  
US-09-513-999C-12063

; Sequence 12063, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.Y.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59,US2,REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 12063  
; LENGTH: 356  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 103  
; OTHER INFORMATION: s=g or c  
US-09-513-999C-12063

Query Match 7.6%; Score 215; DB 4; Length 356;  
Best Local Similarity 100.0%; Pred. No. 5.1e-40;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGGGCTGGCTCTGTCACACAGAGTGCAGTGCAGTGTGATCTTGGCTCATCTGTAAC 67  
Db 142 AGGGCTGGCTCTGTCACACAGAGTGCAGTGCAGTGTGATCTTGGCTCATCTGTAAC 201  
QY 68 TCCACCTCCCGGTTCAAGTATTCATGCTTCAAGCTTCCCGAGTATGGAGATTACAG 127  
Db 202 TCCACCTCCCGGTTCAAGTATTCATGCTTCAAGCTTCCCGAGTATGGAGATTACAG 261  
QY 128 GTGGTGAATTCGAAGATGATCCCGGAGAGAAATGATCCCGAGTGCCTGTCAGAG 187  
Db 262 GTGGTGAATTCGAAGATGATCCCGGAGAGAAATGATCCCGAGTGCCTGTCAGAG 321  
QY 188 CGACACTGTTCTGCTGATGATGCTTCTTCTGCTGCT 222  
Db 322 CGACACTGTTCTGCTGATGATGCTTCTTCTGCTGCT 356

RESULT 4  
US-09-621-976-10391/C  
; Sequence 10391, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jober, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET 054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 10391  
; LENGTH: 354  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 195,280,300  
; OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-10391

Query Match 7.3%; Score 205.2; DB 4; Length 354;  
Best Local Similarity 96.4%; Pred. No. 9e-38;  
Matches 240; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY	1867	GTGAGCTACATCAACCAACCTGAGGCTCTTCAAGCCT -GGTGTCTTGTTCACATGAGCCAT	1925
QY	1867	GTGAGCTACATCAACCAACCTGAGGCTCTTCAAGCCT -GGTGTCTTGTTCACATGAGCCAT	1925
Db	354	GTACGCTACATCAACCAACCTGAGGCTCTTCAAGCCTGAGGATTTCTGTTCAACATGAGCAT	295
QY	1926	GCTAGCCACCATGTGTGTGTCAGATCTGAGGCTGAGCCCCACACCCAAAGGTGCACA	1985
Db	294	GCTAG -CACCATGTGTGTGTCAGATCTT -TGTGTGTGCCCCACACCCAAAGGTGCACA	237
QY	1986	TGTACTGTACATGAGCTGAGGCTCTCAAGCTGAGTCTTGTGAGCTGTGACCTGAGGCTTGATCTT	2045
Db	236	TGTGTGTACATGTGCTGAGGCTCTCAAGCTGTGATCTTGTGAGCTGTGACCTGAGGCTTGATCTT	177
QY	2046	CTCTCTTGTCTTCTGAGCACTTTCAGACTGTGCTCTTACTTCTTTCAGACATCATCACTC	2105
Db	176	CTCTCTTGTCTTCTGAGCACTTTCAGACTGTGCTCTTACTTCTTTCAGACATCATCACTC	117
QY	2106	CTTCCAAAG 2114	
Db	116	CTTCCAAAG 108	

## RESULT 5

US-09-484-970B-17  
; Sequence 17, Application US/09484970B

```

1  GENERAL INFORMATION:
2
3  APPLICANT: Jones, Karen A.
4  APPLICANT: Vollmuth, Wayne
5  APPLICANT: Walker, Michael G.
6  TITLE OF INVENTION: BONE REMODELING GENES
7  FILE REFERENCE: PB-0014 US
8  CURRENT APPLICATION NUMBER: US/09/484,970B
9  CURRENT FILING DATE: 2000-01-18
10 NUMBER OF SEQ ID NOS: 172
11
12 SOFTWARE: PERL Program
13
14 SEQ ID NO 17
15
16 LENGTH: 1651
17
18 TYPE: DNA
19
20 ORGANISM: Homo sapiens
21
22 FEATURE:
23 NAME/KEY: misc feature
24 OTHER INFORMATION: Incyte ID No. 6426186 126510.2CB1
25 NAME/KEY: unsure
26
27 LOCATION: 767-846
28
29 OTHER INFORMATION: a, t, c, g, or other
30
31 US-09-484-970B-17

```

Query Match 4.18; Score 115.4; DB 3; Length 1651;

Best Local Similarity 51.3%; Pred. No. 6.9e-17;  
Matches 337; Conservative 0; Mismatches 296; Indels 24; Gaps 2;

OY	1492	AAAGTGCACATGAACCTGCTGCTGGCCGTCCTTCTCGTCGTGACACAGAGCTTCTGCTTCACG	1551
Db	5	AAGATCCACGTGGCCCTCGGTGGAGCAGCCCTGTCCTCTGAAATCTGAGCCCTTCTTGGTCAT	64
OY	1552	GAGCCGCGTGGCCCTCAGACAGCTCTGAGGCTGGCTCCAGCCAGTGCATCTTCTCTGCAC	1611
Db	65	GTGGGGAATGGCTCAAAAGGGGTCTATGTGCTCTGTGGCCCGGGGGGGCTGTCTTTCAC	124
OY	1612	TTCTCCCTGCTCACTGCTCTTCTCTGATGGGCTTCGAGGGGTAACTCTTACCGAATC	1671
Db	125	TACTTCCTGCTCTGTGGCTTCACTCGAATGGGCTTTGAAGCTTTCACACTTCACTGCTC	184
OY	1672	GTGTGAGAGCTTTTGGACCTATGTCTCTGCTACTCACTCAAGCTGAGCCCATGGGC	1731
Db	185	GCTGTCAAGGTCCTTCAACACCTTACCTTCCGGGCACTACTTCTGAAGCTGAGCTGTGGGGC	244
OY	1732	TGGGGCTTCCCATCTTTCTGTGAGCGCTGTGGGCCCTGTGTGATGTGGAACAATATGGC	1791
Db	245	TGGGGCTCGCCCGCCTGATGTGTATCGGCACTGTGGAGTGGCCAAAGCACTTACGGCTTTAC	304
OY	1792	CCCATCATCTTGTGCTGTGATAGACTCCAGAGGGGCGTCACTA-----CCCT	1831

Db	305	ACCATCCGTATAGGGAGAAACCGACCTCTCTGGAGCTATGCTGTTCCTGGAGGACA	364
QY	1840	TCATGTGCTGATCCGGAACTCCCTGCTCACTAATCAACAACTGGGCTTTTCAGC	1899
Db	365	ACCATGACCCCTCTATATACCGTCCAGGGCTACTTCCTCAACACTTCTCTTTGGC	424
QY	1900	CTGCTGTTTCTGTTCACATGAGCCACTGAGCCACATGAGTGACAGATCCTGGCTG	1958
Db	425	ATGATGATCCTGGCCCTGCTGTGTGAAATCTTCACTCTGTCCCTGCTACAGCGCTC	484
QY	1960	CGCCCCACACCCAAAGTGTCACTATGTGTCACTGTCTGGGCTCAAGCTGTCTT	2019
Db	485	AAGGAGGGGGGAAAGAACCGGAAAGTGTCACTGTCTGGGCTCTCGAGCTGTG	544
QY	2020	GGCCTGCCCTGGGCTTGATCTTTCTCTCTTGTCTGTGCACTTCAGACTGTGTCTC	2079
Db	545	GGTGTGACATGAGGGGTGTGGCCATCTTAC-----CCGGTGGGCTTCCACCC	592
QY	2080	CTTACACCTTTACAGATCATCACTCCCTCAAGGCTTCTCATCTTCACTGTGTAC	2136
Db	593	GCTCAATCTTTGACATTTTCACTCTTGGAGGTGTCTTCACTCTGTCTGTCTC	649

## RESULT 6

US-09-949-016-12226/c  
; Sequence 12226, Application US/09949016

```

? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYOMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: C0001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FASTSEQ for Windows Version 4.0
? SEQ ID NO 12226
?
? LENGTH: 34539
?
? TYPE: DNA
?
? ORGANISM: Human
?
? US-09-949-016-12226

```

Query Match	Score	DB	Length
3.98;	111;	4;	34539;

Best Local Similarity: 86.0%; Pred. No. 2,3e-15;  
Matches 123; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy	7	CAGGGTCTGCCTCTGTCAACAAGGCTGGAATGAGAGTGGTGTATCTCTTGGCTATGCTAAC	66
Db	27949	CAGATTCTCGCTCTGTGTCGCCAAGGCTGGAATGAGAGTGGTGTATCTTGGCTACCGCAAC	278980
Qy	67	CTCAACTCCCCGGGTTCAAGTAATTCAGTCTCAGGCTCCCGAATGACTGGGATTTACA	126
Db	27889	CTTCACCTCCCGGGTTCAACGAAATCTCTTGGCTCAGGCTCTCGAATGACTGAAATTTACA	27830
Qy	127	GGGTGACTTCCAAAGTGACT	149
Db	27829	GGCAACAACCTACAGCGCTGGCT	27807

## RESULT 7

US-09-949-016-13156/c  
; Sequence 13156, Application US/09949016

```

; PATENT NO.: 00000000
;
; GENERAL INFORMATION:
;
; APPLICANT: VENTER, J. Craig et al.
;
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13156  
LENGTH: 34540  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-13156

Query Match 3.9%; Score 111; DB 4; Length 34540;  
Best Local Similarity 86.0%; Pred. No. 2.3e-15;  
Matches 123; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 7 CAGGCTCTGCTCTGTCAACAGGCTGAGTGAAGTGTGATCTTGCTCATGTAAAC 66  
DB 27949 CAGATTCTCGCTCTGCTGCGCCAGGCTGAGTGAAGTGTGATCTTGCTCATCGCAAC 27890  
QY 67 CTCACCTCCCGGGTTCAAGTATCTCATGCTCAGCTCCCGAGTACGGAATTACA 126  
DB 27889 CTCACCTCCCGGGTTCAAGTATCTCTTGCTCAGCTCCCTGAGTACGGAATTACA 27830  
QY 127 GGTGTGACTTCCAGAGTACT 149  
DB 27829 GGCACACATCACCGCTGGCT 27807

RESULT 8  
US-09-146-053-6/c

Sequence 6, Application US/09146053A  
Patent No. 639349  
GENERAL INFORMATION:  
APPLICANT: Ryan, James W.  
APPLICANT: Sprinkle, Terry Joe Curtis  
APPLICANT: Venema, Richard C.  
TITLE OF INVENTION: Human Aminopeptidase P Gene  
FILE REFERENCE: MCG103  
CURRENT APPLICATION NUMBER: US/09/146,053A  
CURRENT FILING DATE: 1998-09-02  
EARLIER APPLICATION NUMBER: 60/057,854  
EARLIER FILING DATE: 1997-09-02  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 6  
LENGTH: 45546  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-146-053-6

Query Match 3.9%; Score 111; DB 3; Length 45546;  
Best Local Similarity 86.0%; Pred. No. 2.5e-15;  
Matches 123; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 7 CAGGCTCTGCTCTGTCAACAGGCTGAGTGAAGTGTGATCTTGCTCATGTAAAC 66  
DB 25748 CAGATTCTCGCTCTGCTGCGCCAGGCTGAGTGAAGTGTGATCTTGCTCATCGCAAC 25689  
QY 67 CTCACCTCCCGGGTTCAAGTATCTCATGCTCAGCTCCCGAGTACGGAATTACA 126  
DB 25688 CTCACCTCCCGGGTTCAAGTATCTCTTGCTCAGCTCCCTGAGTACGGAATTACA 25629  
QY 127 GGTGTGACTTCCAGAGTACT 149  
DB 25628 GGCACACATCACCGCTGGCT 25606

RESULT 9  
US-09-949-016-14573

Sequence 14573, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14573  
LENGTH: 393753  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(393753)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14573

Query Match 3.9%; Score 110.6; DB 4; Length 393753;  
Best Local Similarity 86.5%; Pred. No. 7.2e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGCTCTGCTCTGTCAACAGGCTGAGTGAAGTGTGATCTTGCTCATGTAAAC 68  
DB 145223 GGGCTCTGCTCTGTGCGCCAGGCTGAGTGAAGTGTGATCTTGCTCATGTAAAC 145282  
QY 69 CCACTCCCGGGTTCAAGTATCTCATGCTCAGCTCCCGAGTACGGAATTACA 128  
DB 145283 CCACTCCCGGGTTCAAGTATCTCTTGCTCAGCTCCCTGAGTACGGAATTACA 145342  
QY 129 TGGTGAATCCAGAGTACT 149  
DB 145343 CGCCCGCACACGCTGGCT 145363

RESULT 10  
US-09-949-016-14574

Sequence 14574, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14574  
LENGTH: 393753  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(393753)

OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14574

Query Match 3.9%; Score 110.6; DB 4; Length 391753;  
Best Local Similarity 86.5%; Pred. No. 7.2e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTGACACAGAGTGTGAGTGTGATCTTGGCTCATCTTAACCT 68  
DB 145223 GGGTCTGCTCTGTGACACAGAGTGTGAGTGTGATCTTGGCTCATCTTAACCT 145282  
QY 69 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCTCCGAGTAGCTGGGATTACAG 128  
DB 145283 CCACCTCCCGGGTTCAGAGTATCTCTGCTCAGCTCCGAGTAGCTGGGATTACAG 145342  
QY 129 TGGTACTTCCAGAGTAGCT 149  
DB 145343 CGCCCGCACACGCTGGCT 145363

RESULT 11  
US-09-949-016-14546

Sequence 14546, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14546  
LENGTH: 818128  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(818128)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14546

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTGACACAGAGTGTGAGTGTGATCTTGGCTCATCTTAACCT 68  
DB 569598 GGGTCTGCTCTGTGACACAGAGTGTGAGTGTGATCTTGGCTCATCTTAACCT 569657  
QY 69 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCTCCGAGTAGCTGGGATTACAG 128  
DB 569658 CCACCTCCCGGGTTCAGAGTATCTCTGCTCAGCTCCGAGTAGCTGGGATTACAG 569717  
QY 129 TGGTACTTCCAGAGTAGCT 149  
DB 569718 CGCCCGCACACGCTGGCT 569738

RESULT 12

US-09-949-016-14547  
Sequence 14547, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14547  
LENGTH: 818128  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(818128)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14547

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTGACACAGAGTGTGAGTGTGATCTTGGCTCATCTTAACCT 68  
DB 569598 GGGTCTGCTCTGTGACACAGAGTGTGAGTGTGATCTTGGCTCATCTTAACCT 569657  
QY 69 CCACCTCCCGGGTTCAGAGTATCTCATGCTCAGCTCCGAGTAGCTGGGATTACAG 128  
DB 569658 CCACCTCCCGGGTTCAGAGTATCTCTGCTCAGCTCCGAGTAGCTGGGATTACAG 569717  
QY 129 TGGTACTTCCAGAGTAGCT 149  
DB 569718 CGCCCGCACACGCTGGCT 569738

RESULT 13

US-09-949-016-14548  
Sequence 14548, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 14548  
LENGTH: 818128  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(818128)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14548

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 GGGTCTGCTCTGTGACACAGAGTGTGAGTGTGATCTTGGCTCATCTTAACCT 68



Db 569598 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATCTCGGCTCACTCAACT 569657  
Qy 69 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGATTACAG 128  
Db 569658 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGATTACAG 569717  
Qy 129 TGGTGAATTCGAAGAGTACT 149  
Db 569718 CGCCCGCCACACCGCTGGCT 569738

## RESULT 14

US-09-949-016-14549  
; Sequence 14549, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14549  
; LENGTH: 818128  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(818128)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14549

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 9 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATTTGCTCATGCTCACT 68  
Db 569598 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATTTGCTCATGCTCACT 569657  
Qy 69 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGATTACAG 128  
Db 569658 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGATTACAG 569717  
Qy 129 TGGTGAATTCGAAGAGTACT 149  
Db 569718 CGCCCGCCACACCGCTGGCT 569738

## RESULT 15

US-09-949-016-14550  
; Sequence 14550, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14550  
; LENGTH: 818128  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(818128)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14550

Query Match 3.9%; Score 110.6; DB 4; Length 818128;  
Best Local Similarity 86.5%; Pred. No. 9.5e-15;  
Matches 122; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 9 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATTTGCTCATGCTCACT 68  
Db 569598 GGGTCTGCTCTGTGCGCCAGGCTGAGTGTGATTTGCTCATGCTCACT 569657  
Qy 69 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGATTACAG 128  
Db 569658 CCACCTCCCGGGTTCAAGTATTTCTCATGCTCAAGCTCCCGAGTAAGTGGATTACAG 569717  
Qy 129 TGGTGAATTCGAAGAGTACT 149  
Db 569718 CGCCCGCCACACCGCTGGCT 569738

Search completed: February 12, 2005, 16:47:38  
Job time : 485 secs

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Db	1	CGGCAGCAGGGCTCGCTCTGTCA	CACAGGCTGAGAGTGCAGTGGTGTATCTTGGCTCAT	60
QY	61	CGTAACCTCCACCTCCCGGGTTCA	GTATTCATAGCTCAGCCTCCGAGTAGCTGGG	120
Db	61	CGTAACTTCACCTCCCGGGTTCA	GTATTCATAGCTCAGCCTCCGAGTAGCTGGG	120
QY	121	ATTACAGGTGTGACTTCCAGAGT	AGTATCCGTCGGAGGAAAATGATCTCCCGCAGTGCCTG	180

Db	121	ATTACAGGTGTGATCTTCCAAAGATGACTCCGTCGAGAGAAATGACTCCCAATGTGCTG	180
Qy	181	CTGCAGACGCACTGTGTTCTCTGATGAGTCTGCTCTTCTGTGTCMAAGTGTCCACGGCAG	240
Db	181	CTGCAGACGCACTGTGTTCTCTGATGAGTCTCTCTTCTGTGTCMAAGTGTCCACGGCAG	240
Qy	241	GGCCACAGGGAGAACTTGGCTTCTGAGGCAACGGAAACAGACACACAGAGAGAACCTTC	300
Db	241	GGCCACAGGGAGAACTTGGCTTCTGAGGCAACGGAAACAGACACACAGAGAGAACCTTC	300
Qy	301	CACCTACAAACCCAACACAGACCTGCGCATCTCATGAGAACTCCGAAAGAGCCCTCACA	360
Db	301	CACCTACAAACCCAACACAGACCTGCGCATCTCATGAGAACTCCGAAAGAGCCCTCACA	360
Qy	361	GTCATAGCCCCCTTCCCTGCAGCCCAACCTGTCTTCCGAATCTCTTCCCTGACCCCAAGGGC	420
Db	361	GTCATAGCCCCCTTCCCTGCAGCCCAACCTGTCTTCCGAATCTCTTCCCTGACCCCAAGGGC	420
Qy	421	CTCTACACATCTGTGCGCTCTACTGTGGAACCGAATGTGTGGAGATTACATCTTCTATGAG	480
Db	421	CTCTACACATCTGTGCGCTCTACTGTGGAACCGAATGTGTGGAGATTACATCTTCTATGAG	480
Qy	481	AAGCGTAGCTTCTTGCTGAGTGAACAAAGCCTTAGCTCTCTGTCTTCAGACACAGAG	540
Db	481	AAGCGTAGCTTCTTGCTGAGTGAACAAAGCCTTAGCTCTCTGTCTTCAGACACAGAG	540
Qy	541	GAGAGCTGTGCTAGGGGCCCCCGGTGTGACATCTGTGACCTCTGTGTGAGAGCCCT	600
Db	541	GAGAGCTGTGCTAGGGGCCCCCGGTGTGACATCTGTGACCTCTGTGTGAGAGCCCT	600
Qy	601	CAGAACATCAGCCTGTGCCAGTGCAGCCAGCTTCACTTCTCTTCCAAGTCTCTCCAC	660
Db	601	CAGAACATCAGCCTGTGCCAGTGCAGCCAGCTTCACTTCTCTTCCAAGTCTCTCCAC	660
Qy	661	ACGGCCGCTCAATATGCTCTGTGTGGAACATGTGTGCAAGCTCAAAAGGACCTCCAGCTGTC	720
Db	661	ACGGCCGCTCAATATGCTCTGTGTGGAACATGTGTGCAAGCTCAAAAGGACCTCCAGCTGTC	720
Qy	721	AGCAGATTCCGAAGACATCCCAAGAGAGCTCAAGAGAGCCCTGAGCTGCCCGCCAGC	780
Db	721	AGCAGATTCCGAAGACATCCCAAGAGAGCTCAAGAGAGCCCTGAGCTGCCCGCCAGC	780
Qy	781	CAGCAGTTTGCAGAGCCTGTGAGTGCAGAACTGACTCTGTGAGATTCAATGGGGACATGTGT	840
Db	781	CAGCAGTTTGCAGAGCCTGTGAGTGCAGAACTGACTCTGTGAGATTCAATGGGGACATGTGT	840
Qy	841	TTCCTTCAGAGAGGACCCGATCAAGGCAACGGTATGGAAGCTCCAGGCCACAGCCGAGCTC	900
Db	841	TTCCTTCAGAGAGGACCCGATCAAGGCAACGGTATGGAAGCTCCAGGCCACAGCCGAGCTC	900
Qy	901	CAGAGACTGCACATCACTCCCGCAGAGAGAGAGCAAGACGAGATCATGAGTACTCG	960
Db	901	CAGAGACTGCACATCACTCCCGCAGAGAGAGAGCAAGACGAGATCATGAGTACTCG	960
Qy	961	GTCGTGCTGTGCTCCGAACCTTCTTCAGAGACGAAAGGCCGAGACGGGGAGAGCTGAGAA	1020
Db	961	GTCGTGCTGTGCTCCGAACCTTCTTCAGAGACGAAAGGCCGAGACGGGGAGAGCTGAGAA	1020
Qy	1021	AGACTCTCTCTGTGTGATCTTTCAGAGACCAAGCCCTGTTCAGAGACAAGAAATTCAGGCAA	1080
Db	1021	AGACTCTCTCTGTGTGATCTTTCAGAGACCAAGCCCTGTTCAGAGACAAGAAATTCAGGCAA	1080
Qy	1081	GTCCTGTGGTGAAGAGTCTTGGGGATTGTGTGACAGAACCAAGTATGCCAATCTCAGC	1140
Db	1081	GTCCTGTGGTGAAGAGTCTTGGGGATTGTGTGACAGAACCAAGTATGCCAATCTCAGC	1140
Qy	1141	GAGCCCGTGTGATCACTTTCAGAGACAGGCTACAGCCGAGAAATGTGACTCTGCATATGT	1200
Db	1141	GAGCCCGTGTGATCACTTTCAGAGACAGGCTACAGCCGAGAAATGTGACTCTGCATATGT	1200
Qy	1201	GTTGTTCTGAGTTGAAGACCCCAATTGAGACAGCCCGGGCATTTGAGACAGTGTGGGTGT	1260

Db	1201	GTGTTCTGGGGTTGAAGACCCCAATTGAGACAGCCGGGGCAATTGGAGCAGTGTGGGGT	1260
Qy	1261	GAGACCGTCAGAGAGAGAAACCCAAACATCTCTGTTCTGCAACCACTTTGACTCTTTGCA	1320
Db	1261	GAGACCGTCAGAGAGAGAAACCCAAACATCTCTGTTCTGCAACCACTTTGACTCTTTGCA	1320
Qy	1321	GTGCTGATAGTCTACCTCGAGAGAGTGAAGCCGCTGCACAAGCACTACCTGAGCTCTCTC	1380
Db	1321	GTGCTGATAGTCTCTCTCGAGAGAGTGAAGCCGCTGCACAAGCACTACCTGAGCTCTCTC	1380
Qy	1381	TCCACGTGGGCTGTGTGCTCTCTGCGCTGAGCTGCTTGTCAACAATTGGCGCTTACTCTC	1440
Db	1381	TCCACGTGGGCTGTGTGCTCTCTGCGCTGAGCTGCTTGTCAACAATTGGCGCTTACTCTC	1440
Qy	1441	TGCTCCAGGGTGGCCCGCCGTCGACAGAGAGAAACCTCGGGACAACAACATCAAGGTGCAC	1500
Db	1441	TGCTCCAGGGTGGCCCGCCGTCGACAGAGAGAAACCTCGGGACAACAACATCAAGGTGCAC	1500
Qy	1501	ATGAACCTGTGCTGGGCGCTCTTCTCTGTGACACAGAGCTCTCTGTCAAGCAGCCGATG	1560
Db	1501	ATGAACCTGTGCTGGGCGCTCTTCTCTGTGACACAGAGCTCTCTGTCAAGCAGCCGATG	1560
Qy	1561	GCCCTGACAGGCTCTGAGGCTGTGCTGCCAGGCCAGTGCATCTTCTGTGACTTCTCCCG	1620
Db	1561	GCCCTGACAGGCTCTGAGGCTGTGCTGCCAGGCCAGTGCATCTTCTGTGACTTCTCCCG	1620
Qy	1621	CTGACCGGCTTCTCTGATAGGCGCTCGAGGGGTGACAACCTTACCCGACTGTGTGAG	1680
Db	1621	CTGACCGGCTTCTCTGATAGGCGCTCGAGGGGTGACAACCTTACCCGACTGTGTGAG	1680
Qy	1681	GTCTTTGGCACTATATGCTCCGTGGCTATCTAATAAGTGAAGCCCAAGGCTGGGGCTTC	1740
Db	1681	GTCTTTGGCACTATATGCTCCGTGGCTATCTAATAAGTGAAGCCCAAGGCTGGGGCTTC	1740
Qy	1741	CCCATCTTTCTGTGAGACGCTGTGTGGCCCTGTGTGATGTGACAACTATGGCCCCATCATC	1800
Db	1741	CCCATCTTTCTGTGAGACGCTGTGTGGCCCTGTGTGATGTGACAACTATGGCCCCATCATC	1800
Qy	1801	TTGGCTGTGATAGAACTCAAGAGGCGTCACTACCTTCCATGTGTGGATCCGGGAGC	1860
Db	1801	TTGGCTGTGATAGAACTCAAGAGGCGGTCACTACCTTCCATGTGTGGATCCGGGAGC	1860
Qy	1861	TCCCGGTGACATCAATCAACCACTGAGGCTCTTCAAGCTGTGTGTCTGTTCACATGT	1920
Db	1861	TCCCGGTGACATCAATCAACCACTGAGGCTCTTCAAGCTGTGTGTCTGTTCACATGT	1920
Qy	1921	GCCATGTAGCCACCATGTGTGTGACATCTCTGCGCTGCGGCCCAACCCCAAAAGTGG	1980
Db	1921	GCCATGTAGCCACCATGTGTGTGACATCTCTGCGCTGCGGCCCAACCCCAAAAGTGG	1980
Qy	1981	TCACATGTGTGACATCTGTGTGGGCTGACGCTGTGCTTGTGAGGCTGTGATC	2040
Db	1981	TCACATGTGTGACATCTGTGTGGGCTGACGCTGTGCTTGTGAGGCTGTGATC	2040
Qy	2041	TTCCTCTCTTGTGCTTCTGAGCACTTCAAGCTTGTGTCTTACCTTTCAAGATCATC	2100
Db	2041	TTCCTCTCTTGTGCTTCTGAGCACTTCAAGCTTGTGTCTTACCTTTCAAGATCATC	2100
Qy	2101	ACCTCTCTTCAAGGCTTCTCATCTTCAATCTGTATCTGTATCAATGAGCGGTGTGATC	2160
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Qy	2161	GGTGGGCCCTCCCTCTGAGAGCACTCAAGCTTGTGTGTGTCTTCAAGTGTGATGACAGAG	2220
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Qy	2221	AGCACTGTGTCAAGCGCTCTAAGGCTTCAAGCCCACTGTGCAATGTATGAACAGAGAG	2280
Db	2221	AGCACTGTGTCAAGCGCTCTAAGGCTTCAAGCCCACTGTGCAATGTATGAACAGAGAG	2280
Qy	2281	TGGGCGCTGTGACACATGTGTGGCGCCCGAGCCAGGCCCAAGGCCAGGCTCAG	2340
Db	2281	TGGGCGCTGTGACACATGTGTGGCGCCCGAGCCAGGCCCAAGGCCCAAGGCTCAG	2340



Db 1201 GTGTTCTGGGTTGAAGAACCCCATTTGAGCAGCCCGGCGCATTTGAGCGTCTGGTGT 1260  
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Db 1261 GAGACCGGTGAGGAGGAAACCCAAATCTGCTCTTCTGCAACCATTTGACTTTTGA 1320  
Qy 1321 GTGCTGATGATCTCTCGGTGAGGTGAGCGCCGTGCAACAGCACTTCTGAGCTCTG 1380  
Db 1321 GTGCTGATGATCTCTCGGTGAGGTGAGCGCCGTGCAACAGCACTTCTGAGCTCTG 1380  
Qy 1381 TCTTACGTGGGCTGTGTGTCTGTCTGCGCTGCTGCTTGTCAACATTTGCCCTTAC 1440  
Db 1381 TCTTACGTGGGCTGTGTGTCTGTCTGCGCTGCTGCTTGTCAACATTTGCCCTTAC 1440  
Qy 1441 TCTTACGTGGGCTGTGTGTCTGTCTGCGCTGCTGCTTGTCAACATTTGCCCTTAC 1500  
Db 1441 TCTTACGTGGGCTGTGTGTCTGTCTGCGCTGCTGCTTGTCAACATTTGCCCTTAC 1500  
Qy 1501 ATGAACTGTCTGTGCGCTGTCTTCTGCTGAGCAACAGCTTCTGTCTGAGCGCGGTG 1560  
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Qy 1621 CTACCTGCTTCTCTGAGTGGGCTCTGAGGCGTCAACCTTCAACGACTCTGTGTGAG 1680  
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Db 1801 TTGGCTGTGCTAGACTCCAGAGGCGTCTTACTTCACTGAGCGCCCAATGGGCGCTT 1860  
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Db 1861 TCCCTGTGCTAGACTCCAGAGGCGTCTTACTTCACTGAGCGCCCAATGGGCGCTT 1920  
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Db 1921 GCGATGCTAGCACTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1980  
Qy 1981 TCAATGTGTGCACTGTGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 2040  
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Qy 2041 TTTCTTCTCTGTGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 2100  
Db 2041 TTTCTTCTCTGTGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 2100  
Qy 2101 ACCTCTCTCAAGGCTCTCTCATCTTGTGATGTGATGTGATGTGATGTGATGTGATGT 2160  
Db 2101 ACCTCTCTCAAGGCTCTCTCATCTTGTGATGTGATGTGATGTGATGTGATGTGATGT 2160  
Qy 2161 GGTGGGCGCTCTCTCTGAGAGCACTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 2220  
Db 2161 GGTGGGCGCTCTCTCTGAGAGCACTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 2220  
Qy 2221 AGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280  
Db 2221 AGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280  
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Db 2281 TGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340

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Db 2341 CCGAGACTTTTGAAGAGCCCAACGACATGAGAGATGAGGCGCTTGTGCAATGTGAGAGGA 2400  
Qy 2401 CTCCCGGCGCTGTGGGCTTTTGAATTTGAGCTTTGAGGACTTCTGAGCTCTCACTGAGCTCC 2460  
Db 2401 CTCCCGGCGCTGTGGGCTTTTGAATTTGAGCTTTGAGGACTTCTGAGCTCTCACTGAGCTCC 2460  
Qy 2461 ACGGACTCAGAGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2520  
Db 2461 ACGGACTCAGAGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2520  
Qy 2521 CAGCTGAGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 2580  
Db 2521 CAGCTGAGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 2580  
Qy 2581 GCGCTTGTGATCTTGAAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 2640  
Db 2581 GCGCTTGTGATCTTGAAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 2640  
Qy 2641 TGTGCTCTGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2700  
Db 2641 TGTGCTCTGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2700  
Qy 2701 TTTTAACTCTGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2760  
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Qy 2821 CG 2822  
Db 2821 CG 2822

RESULT 3  
US-10-073-054-1  
; Sequence 1, Application US/10073054  
; Publication No. US20030167485A1  
; GENERAL INFORMATION:  
; APPLICANT: Garvan Institute of Medical Research  
; APPLICANT: HERZOG, Herbert  
; TITLE OF INVENTION: No. US20030167485A1 G-protein coupled receptor-encoding gene  
; FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
; CURRENT APPLICATION NUMBER: US/10/073,054  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US 09/308,696  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR APPLICATION NUMBER: PCT/AU98/00805  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: AU P09386  
; PRIOR FILING DATE: 1997-09-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2822  
; TYPE: DNA  
; ORGANISM: Human GPR56-1 (TSR32)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (163)..(2241)  
; OTHER INFORMATION:  
US-10-073-054-1

Query Match 100.0%; Score 2822; DB 16; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 CGGACGAGGAGTCTCGCTCTGTCACA CAGGCTGGAAGTCAGTGTGATCTTGGCTCAT 60  
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QY 61 CGTAACTTCACACCTCCGGGTTCAAGTATCTCATGCTTCAGGCTCCGAGTAGCTGGG 120  
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QY 121 ATTAAGAGTGTGATCTTCAAGATGATCTCCGTGAGGAAATGATCTCCCAAGTGGCTG 180  
DB 121 ATTAAGAGTGTGATCTTCAAGATGATCTCCGTGAGGAAATGATCTCCCAAGTGGCTG 180  
QY 181 CTGACAGAGCAGACGTCTCGTGTGAGTGTGCTCTTCTGTGCTCAAGGTTGCCACGAGAG 240  
DB 181 CTGACAGAGCAGACGTCTCGTGTGAGTGTGCTCTTCTGTGCTCAAGGTTGCCACGAGAG 240  
QY 241 GGGCACAAGGAGAGCTTTCGCTTCTGAGCCAGCCAGGAAACAGACACA CAGAGAGAGCTTC 300  
DB 241 GGGCACAAGGAGAGCTTTCGCTTCTGAGCCAGCCAGGAAACAGACACA CAGAGAGAGCTTC 300  
QY 301 CACTACAAACCCACACAGACCTGCGATCTTCATTCGAGAACTCCGAGAGAGCCCTGACA 360  
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QY 361 GTCCATGCCCCCTTCCGTCAGAGCCACCCCTGCTCCGATCTTCCCTGACCCGAGAGGAC 420  
DB 361 GTCCATGCCCCCTTCCGTCAGAGCCACCCCTGCTCCGATCTTCCCTGACCCGAGAGGAC 420  
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DB 421 CTCTACCACTTCTGCTCTCTACTGAGAACGACATGCTGGAGATTAATCTTCTCTATGAC 480  
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DB 481 AAGGTAATCTTCTGCTGAGTGA CAAGACCTGAGCCCTCTGCTTCAGAGACAGAGAG 540  
QY 541 GAGAGCTGGCTCAGAGGCCCCCGCTGTAGGCACTTCTGTGACCTCTCTGTGAGAGCCCT 600  
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DB 661 ACGGCGCTCAAAAGCTCCGCTGTGAGCAATGTGAGGCTCAAAAGGAGCTTCCAGGCTGCT 720  
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DB 1381 TCCATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
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DB 1621 CTACCTGCTCTTCTGAGTGGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
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US-10-460-479-1  
; Sequence 1, Application US/10460479  
; Publication No. US20040093627A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenand, John Charles  
; APPLICANT: Hart, Kevin Anthony  
; TITLE OF INVENTION: Methods GPR56  
; FILE REFERENCE: 1991-220  
; CURRENT APPLICATION NUMBER: US/10/460,479  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: 09/845,771  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,422  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 2822  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-460-479-1

Query Match 100.0%; Score 2822; DB 17; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
US-10-295-027-767  
Sequence 767, Application US/10295027  
Publication No. US2003022350A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Glyme, Richard  
APPLICANT: Hevezi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394

PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO: 767  
LENGTH: 2821  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-295-027-767

Query Match 99.9%; Score 2820; DB 17; Length 2821;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2461 AGGAGACTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 2520  
Qy 2521 CCAAGTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2580  
Db 2521 CCAAGTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2580  
Qy 2581 GGCCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2640  
Db 2581 GGCCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2640  
Qy 2641 TGTGCTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2700  
Db 2641 TGTGCTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2700  
Qy 2701 TTTTAACTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 2760  
Db 2701 TTTTAACTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 2760  
Qy 2761 CCGTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2820  
Db 2761 CCGTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGT 2820

RESULT 6  
US-09-814-353-20017

Sequence 20017, Application US/09814353  
Publication No. US20030165831A1  
GENERAL INFORMATION:  
APPLICANT: Lee, John  
APPLICANT: Thompson, Pamela  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
THERAPY OF OVARIAN CANCER  
FILE REFERENCE: MRI-006B  
CURRENT APPLICATION NUMBER: US/09/814,353  
PRIOR APPLICATION NUMBER: US 2001-03-21  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/207,124  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 60/211,940  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,820  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 60/220,661  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/257,672  
NUMBER OF SEQ ID NOS: 22037  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20017  
LENGTH: 3902  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1, 2, 3898, 3899, 3900, 3901, 3902  
OTHER INFORMATION: n = A,T,C or G  
US-09-814-353-20017  
Query Match 98.7%; Score 2785.4; DB 10; Length 3902;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2812; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
Qy 2 GGCAGAGGAGTCTCCCTCTGTGACACAGGCTGAGTGTGATCTTGTGCTGATC 61  
Db 304 GGCAGAGGAGTCTCCCTCTGTGACACAGGCTGAGTGTGATCTTGTGCTGATC 363  
Qy 62 GTAACTTCACTCCCGGTTCAAGTATTCAGGCTTCCAGAGTGTGCTGCTG 121  
Db 364 GTAACTTCACTCCCGGTTCAAGTATTCAGGCTTCCAGAGTGTGCTGCTG 423  
Qy 122 TTAAGAGTGTGATCTTCAAGAGTACTCGTGTGAGGAAATGATCTCCAGTGTG 181  
Db 424 TTAAGAGTGTGATCTTCAAGAGTACTCGTGTGAGGAAATGATCTCCAGTGTG 483  
Qy 182 TGCAGAGCACTGTCTGTGAGTGTGCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 241  
Db 484 TGCAGAGCACTGTCTGTGAGTGTGCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 543  
Qy 242 GCCAGAGGAACTTTCGTTTGTGAGCCAGGGAACAGACACAGAGAGGCTTCC 301  
Db 544 GCCAGAGGAACTTTCGTTTGTGAGCCAGGGAACAGACACAGAGAGGCTTCC 603  
Qy 302 ACTTAAACCAACCAACCAACCACTGTGATCTTCAATGAGAACTCCGAAAGGCTTCA 361  
Db 604 ACTTAAACCAACCAACCAACCACTGTGATCTTCAATGAGAACTCCGAAAGGCTTCA 663  
Qy 362 TCCATGCCCCCTTCTCTGAGCCGACCTGCTTCCGATCTTCCGATCTTCCGATCTTCC 421  
Db 664 TCCATGCCCCCTTCTCTGAGCCGACCTGCTTCCGATCTTCCGATCTTCCGATCTTCC 723  
Qy 422 TCTAACCTTGTGCTTCACTGAAACCGAATGTGTGAGGATTAATCTTCTATGGA 481  
Db 724 TCTAACCTTGTGCTTCACTGAAACCGAATGTGTGAGGATTAATCTTCTATGGA 783  
Qy 482 AGCGTGAATCTTGTGAGTGAACCAAGCTTCACTCTCTGCTTCAAGACACAGAGG 541



DB 784 AGCGGACCTTCTGAGTGAACAAGCTTAGCTCTGCTTCCAGACACAGAGG 843  
OY 542 AGAGCTGGCTCAAGGCCCCCGCTGTATAGCACTTCTGTACCTCCCTGTGGAGCCCTC 601  
DB 844 AGAGCTGGCTCAAGGCCCCCGCTGTATAGCACTTCTGTACCTCCCTGTGGAGCCCTC 903  
OY 602 AGAATATAGAGCTGGCCAGAGCCGAGCTTCACTTCTCTTCCAGAGTCTCTCCACA 661  
DB 904 AGAATATAGAGCTGGCCAGAGCCGAGCTTCACTTCTCTTCCAGAGTCTCTCCACA 963  
OY 662 CGGCGCTCAACATGCTGTGGTGAACATGTGGAGCTCAAAAGGAGCTTCCAGCTGTCA 721  
DB 964 CGGCGCTCAACATGCTGTGGTGAACATGTGGAGCTCAAAAGGAGCTTCCAGCTGTCA 1023  
OY 722 GCGAGTCTGTAAGATCCCGAGAGGCTCAAGAGGAGCTCGGCTGGCCCCGAGCC 781  
DB 1024 GCGAGTCTGTAAGATCCCGAGAGGCTCAAGAGGAGCTCGGCTGGCCCCGAGCC 1083  
OY 782 AGCAGTTGCAAGAGCTGAGAGTGAACCTGACTGTGAGATTCAATGGGGAGCATGTGT 841  
DB 1084 AGCAGTTGCAAGAGCTGAGAGTGAACCTGACTGTGAGATTCAATGGGGAGCATGTGT 1143  
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DB 1144 CCTTGAAGAGAGACCGGATCAACGCGCATATGGAAGTCCAGGCCACAGCCGCGCTCC 1203  
OY 902 AGGACCTGCAATCCACTCCCGGAGAGAGAGAGAGAGAGAGATCATAGAGTACTCG 961  
DB 1204 AGGACCTGCAATCCACTCCCGGAGAGAGAGAGAGAGAGAGATCATAGAGTACTCG 1263  
OY 962 TGTCTGTGCTGAACACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021  
DB 1264 TGTCTGTGCTGAACACTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323  
OY 1022 GACTCTCTGTGAGACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081  
DB 1324 GACTCTCTGTGAGACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383  
OY 1082 TCTGTGGTGAAGAGCTTGGGGATTTGTGTACAGAACCAAGATGAGCACTCACGG 1141  
DB 1384 TCTGTGGTGAAGAGCTTGGGGATTTGTGTACAGAACCAAGATGAGCACTCACGG 1443  
OY 1142 AGCCCTGTGTCTCACTTTCAGACACAGCTACAGCCGAGAGATGTGACTCTGCAATG 1201  
DB 1444 AGCCCTGTGTCTCACTTTCAGACACAGCTACAGCCGAGAGATGTGACTCTGCAATG 1503  
OY 1202 TGTCTGTGGTGAAGAGCCCAATTTGAGAGAGCCGAGGAGATTTGAGAGAGTGTG 1261  
DB 1504 TGTCTGTGGTGAAGAGCCCAATTTGAGAGAGCCGAGGAGATTTGAGAGAGTGTG 1563  
OY 1262 AGACCGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321  
DB 1564 AGACCGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623  
OY 1322 TGTCTGTGGTGAAGAGCCCAATTTGAGAGAGCCGAGGAGATTTGAGAGAGTGTG 1381  
DB 1624 TGTCTGTGGTGAAGAGCCCAATTTGAGAGAGCCGAGGAGATTTGAGAGAGTGTG 1683  
OY 1382 CCTAGGTGGAGTGTGTCTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1441  
DB 1684 CCTAGGTGGAGTGTGTCTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1743  
OY 1442 GCTTCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1501  
DB 1744 GCTTCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1803  
OY 1502 TGAACCTGTGCTGAGCGCTCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1561  
DB 1804 TGAACCTGTGCTGAGCGCTCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1863  
OY 1562 CCTTGAAGAGCTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1621

DB 1864 CCTTGAAGAGCTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1923  
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DB 1924 TCACCTGCTTCTGTGATGGGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1983  
OY 1682 TCTTGTGAGAGCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1741  
DB 1984 TCTTGTGAGAGCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2043  
OY 1742 CCATCTTCTGTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1801  
DB 2044 CCATCTTCTGTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2103  
OY 1802 TGTGTGTGATGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1861  
DB 2104 TGTGTGTGATGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2163  
OY 1862 CCTTGTGAGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1921  
DB 2164 CCTTGTGAGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2223  
OY 1922 CCATGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1981  
DB 2224 CCATGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2283  
OY 1982 CACATGTGCTGATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2041  
DB 2284 CACATGTGCTGATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2343  
OY 2042 TCTTCTGCTTGTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2101  
DB 2344 TCTTCTGCTTGTGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2403  
OY 2102 CCTCTTCAAGAGAGCTTCTGATCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2161  
DB 2404 CCTCTTCAAGAGAGCTTCTGATCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2463  
OY 2162 GTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2221  
DB 2464 GTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2523  
OY 2222 GCACTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2281  
DB 2524 GCACTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2583  
OY 2282 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2341  
DB 2584 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2643  
OY 2342 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2401  
DB 2644 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2703  
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DB 2704 TCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2761  
OY 2462 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2521  
DB 2762 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2821  
OY 2522 CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
DB 2822 CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2881  
OY 2581 GAGCTTGAATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640  
DB 2882 GAGCTTGAATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2941  
OY 2641 TGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
DB 2942 TGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3001

Qy 2701 TTTTAACCTGAGTGGACCAAGGCGGCGGACGACTTTCAGGGCCAGAG 2760  
Db 3002 TTTTAACCTGAGTGGACCAAGGCGGCGGCGGACGACTTTCAGGGCCAGAG 3061  
Qy 2761 CCCTGGCGGAGAGAGGCGCTTTGGCAGAGACAGAGAGCTTGCTTACCTTGAGCC 2820  
Db 3062 CCCTGGCGGAGAGAGGCGCTTTGGCAGAGACAGAGAGCTTGCTTACCTTGAGCC 3121  
Qy 2821 C 2821  
Db 3122 C 3122

RESULT 7  
US-09-978-295A-482  
Sequence 482, Application US/09978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Boetsch, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerder, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
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PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-25  
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PRIOR FILING DATE: 1998-03-26  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
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 PRIOR APPLICATION NUMBER: 60/082797  
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 PRIOR FILING DATE: 1998-04-23  
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 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.6%; Score 2783.4; DB 9; Length 3819;  
 Best Local Similarity 99.7%; Pred. No. 0;

Matches	2810;	Conservative	0;	Mismatches	6;	Indels	3;	Gaps	2;
QY	4	CAGCAGGCTCTGCTCTGTCACACAGCTGAGTGTGATCTTTGGCTCATCTCT							63
DB	55	CTGAGAGGCTCTGCTCTGTCACACAGCTGAGTGTGATCTTTGGCTCATCTCT							114
QY	64	AACCTTCACTCTCCGGGTTCAAGTATTCATGCTCAGCTCCGAGTATGCTGGATT							123
DB	115	AACCTTCACTCTCCGGGTTCAAGTATTCATGCTCAGCTCCGAGTATGCTGGATT							174
QY	124	ACAGTGTGACTTCCAAAGTGTACTCCGTGAGAGAAATGACTCTCCAGTCTGCTG							183
DB	175	ACAGTGTGACTTCCAAAGTGTACTCCGTGAGAGAAATGACTCTCCAGTCTGCTG							234
QY	184	CAGACGACACTGTTCTGCTGATGCTCTTCTGCTGCAAGTGTCCAGGAGGAGC							243
DB	235	CAGACGACACTGTTCTGCTGATGCTCTTCTGCTGCAAGTGTCCAGGAGGAGC							294
QY	244	CACAGGGAAGACTTGTGCTTCTGACAGCAGCAGAACACACACACAGAGCCTCAC							303
DB	295	CACAGGGAAGACTTGTGCTTCTGACAGCAGCAGAACACACACACAGAGCCTCAC							354
QY	304	TACAAACCAACACACACACTGCGCATCTCATGAGAACTCCGAAAGGCTTCAAGTC							363
DB	355	TACAAACCAACACACACACTGCGCATCTCATGAGAACTCCGAAAGGCTTCAAGTC							414
QY	364	CATGCCCCCTTCTGCTGAGCCCACTCCGCTTCCGATCTTCCCTGACCCCAAGGAGCTC							423
DB	415	CATGCCCCCTTCTGCTGAGCCCACTCCGCTTCCGATCTTCCCTGACCCCAAGGAGCTC							474
QY	424	TACCACTTGTGCTCTACTGGAACCGACATGCTGGAGATTAATCTTCTTATGGCAAG							483
DB	475	TACCACTTGTGCTCTACTGGAACCGACATGCTGGAGATTAATCTTCTTATGGCAAG							534
QY	484	CGTGACTTCTTGTGATGACAAAGCTCTAGCTCTCTGCTTCCAGACACAGAGAG							543
DB	535	CGTGACTTCTTGTGATGACAAAGCTCTAGCTCTCTGCTTCCAGACACAGAGAG							594
QY	544	AGCTGTGCTAGGGGCCCCCGCTGTAGGACCTCTGTCACCTCTGAGGAGCCCTCAG							603
DB	595	AGCTGTGCTAGGGGCCCCCGCTGTAGGACCTCTGTCACCTCTGAGGAGCCCTCAG							654
QY	604	AACATCAGCCTGCCAGTGCAGCCAGCTTCTCTTCCATCAAGTCTCTCCACAGC							663
DB	655	AACATCAGCCTGCCAGTGCAGCCAGCTTCTCTTCCATCAAGTCTCTCCACAGC							714
QY	664	GCCGCTCAATGCTCTGATGACATGTCGACGTTCAAAAGGAACTTCAAGTCTCAGC							723
DB	715	GCCGCTCAATGCTCTGATGACATGTCGACGTTCAAAAGGAACTTCAAGTCTCAGC							774
QY	724	CAGTTCTGAAAGCATCCCAAGAGGCTCAAGAGGCTCTGAGCTCCCGCCAGCCAG							783
DB	775	CAGTTCTGAAAGCATCCCAAGAGGCTCAAGAGGCTCTGAGCTCCCGCCAGCCAG							834
QY	784	CAGTTGCAAGCCTGAGTGTCAAACTGACTCTGTGATTCATGGGGGAATATGTGTCC							843
DB	835	CAGTTGCAAGCCTGAGTGTCAAACTGACTCTGTGATTCATGGGGGAATATGTGTCC							894
QY	844	TTTGAAGAGACCGGATTAAGCCACGGTATGGAAGCTCCAGCCACAGCGGCTCCAG							903
DB	895	TTTGAAGAGACCGGATTAAGCCACGGTATGGAAGCTCCAGCCACAGCGGCTCCAG							954
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC27  
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APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
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## RESULT 10

US-09-999-832A-482  
Sequence 482, Application US/0999832A  
Publication No. US20020192706A1

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APPLICANT: Baker Kevin P.  
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APPLICANT: Filvaroff, Ellen  
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APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerltisen, Mary E.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30

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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.6%; Score 2783.4; DB 9; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0; Mismatches 6; Indels 3; Gaps 2;  
Matches 2810; Conservative 0

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55 CTGAGAGGCTCTGCTCTGTCACAGAGCTGAGTGCATGTGTGATCTTGGCTCATGCT 114

64 AACCTCCACTCCCGGGTTCAAGTATTTCTATGCTTCAAGCTTCCCGAGTGGGATT 123  
115 AACCTCCACTCCCGGGTTCAAGTATTTCTATGCTTCAAGCTTCCCGAGTGGGATT 174

124 AACGCTGTGACTTCCAGAGTGAATCCGTGAGAGAAATGACTCCCAAGTGGCTGTG 183  
175 AACGCTGTGACTTCCAGAGTGAATCCGTGAGAGAAATGACTCCCAAGTGGCTGTG 234

184 CAGACGACATGTTCTGCTGATGATGCTGCTTCTGCTGTCAGAGTCCCAAGGAGGAG 243  
225 CAGACGACATGTTCTGCTGATGATGCTGCTTCTGCTGTCAGAGTCCCAAGGAGGAG 294

244 CACAGGAGAACTTTCGCTTTCGAGCGAGGAGAAACAGACACAGAGAGAGCTTCCAC 303  
295 CACAGGAGAACTTTCGCTTTCGAGCGAGGAGAAACAGACACAGAGAGAGCTTCCAC 354

304 TACAACCCACACAGACCTGCGCATCTCATGAGAACTCGAAGAGGCTCTCAAGTC 363  
355 TACAACCCACACAGACCTGCGCATCTCATGAGAACTCGAAGAGGCTCTCAAGTC 414

364 CATGCCCTTTTCCCTGAGCCCACTGCTTCCGATCTTCCCTGACCCCGAGGAGCTTC 423  
415 CATGCCCTTTTCCCTGAGCCCACTGCTTCCGATCTTCCCTGACCCCGAGGAGCTTC 474

424 TACCACTTCTGCTTACTGGAACCGAATGCGGAGATTACATCTTCTCTATGGCAAG 483  
475 TACCACTTCTGCTTACTGGAACCGAATGCGGAGATTACATCTTCTCTATGGCAAG 534

484 CGTGACTTCTGCTGATGAGCAAAAGCTTACCTCTCTGCTTCAAGACCAAGAGAG 543  
535 CGTGACTTCTGCTGATGAGCAAAAGCTTACCTCTCTGCTTCAAGACCAAGAGAG 594

544 AGCTTGCTCAGAGGCCCCCGCTGTTAGCACTTCTGTCACCTCTGAGAGAGCTTCAG 603  
595 AGCTTGCTCAGAGGCCCCCGCTGTTAGCACTTCTGTCACCTCTGAGAGAGCTTCAG 654

604 AACATCAGCTGCTCCAGTGCAGGCTTCACTTCTGCTTCAAGTCTTCCCAAGCAG 663  
655 AACATCAGCTGCTCCAGTGCAGGCTTCACTTCTGCTTCAAGTCTTCCCAAGCAG 714

664 GCGCTCAATGCTCTGCTGAGCATGTCGAGCTCAAAAGGAGCTTCCAGTGCCTCAG 723  
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724 CAGTTCCTGAAGCATTCCTGAGAGGCTTCAAGAGGAGGCTTCCAGTGCCTCAG 783  
775 CAGTTCCTGAAGCATTCCTGAGAGGCTTCAAGAGGAGGCTTCCAGTGCCTCAG 834



APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
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APPLICANT: Fong, Sherman  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
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Query Match 98.6%; Score 2783.4; DB 10; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
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## RESULT 12

US-09-978-608A-482

Sequence 482, Application US/09978608A  
Publication No. US20030045462A1

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APPLICANT: Hillan, Kenneth J.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P26301C22  
CURRENT FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File wrapper or Palm  
SEQ ID NO 482  
LENGTH: 3819  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-978-608A-482

Query Match 98.6%; Score 2783.4; DB 10; Length 3819;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;  
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APPLICANT: Fong, Sherman  
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APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: US/09/978,191A  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500





Db 1495 TTCAGGGTGGCCCTGCGGTGACAGAGAAACCTCGGACCTAACACATCAAGGTGACATG 1554  
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Qy 1684 TTGGGACCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1743  
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Qy 1864 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923  
Db 1915 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1974  
Qy 1924 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1983  
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Qy 2164 GGCCCTCTCTCTGAGAGGAGTCTGAGTGGCGCAGGCTGCCATCAGCTCGGCGAGC 2223  
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Qy 2763 CTGGCGGAGGAGGCGGCTTGGCGAGGAGCAGGAGGCTGCGCTGAGCTCTGAGGCC 2821  
Db 2813 CTGGCGGAGGAGGCGGCTTGGCGAGGAGCAGGAGGCTGCGCTGAGGCC 2871

## RESULT 15

US-09-978-403A-482

Sequence 482, Application US/09978403A  
Publication No. US2003050240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austen L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James F.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC17  
CURRENT FILING DATE: 2002-03-19  
CURRENT APPLICATION NUMBER: US/09/978,403A  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
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71	PRIOR APPLICATION NUMBER: 60/085573
72	PRIOR FILING DATE: 1998-05-15
73	PRIOR APPLICATION NUMBER: 60/085704

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.6%; Score 2783.4; DB 10; Length 3819;

Best Local Similarity 99.7%; Pred. No. 0; Mismatches 6; Indels 3; Gaps 2;

Matches 2810; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

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55 CTGAGAGGCTCGCTCTGTCA CACAGGCTGAGTGTGATCTTGGCTCATCTG 114  
64 AACCTCAACCTCCGGGTTCAAGTATCTATGCTTCCGAGTATGGAGAT 123  
115 AACCTCAACCTCCGGGTTCAAGTATCTATGCTTCCGAGTATGGAGAT 174  
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484 CTGATCTTCTGTGAGTGA CAAAGCTTGAAGCTTCTGTGCTTCAAGACAGAGAG 543  
535 CTGATCTTCTGTGAGTGA CAAAGCTTGAAGCTTCTGTGCTTCAAGACAGAGAG 594  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:21:49 / Search time 8945 Seconds  
(without alignments)  
12008.649 Million cell updates/sec

Title: US-10-073-054-1

Perfect score: 2822  
Sequence: 1 cgcgcagcagggctcgcctc.....ctcgcctaccctcgcgcgcg 2822

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	2737.6	97.0	3835	3 BC013207	BC013207 Homo sapi
2	1437.4	50.9	3295	3 AK087268	AK087268 Mus muscu
3	909.6	32.2	966	5 BX381703	BX381703 BX381703
4	904	32.0	971	5 BX417949	BX417949 BX417949
5	852.6	30.2	941	5 BX384045	BX384045 BX384045
6	844.6	29.9	981	5 BX339034	BX339034 BX339034
7	843.2	29.9	932	5 BU183659	BU183659 AGENCOURT
8	842.8	29.9	965	5 BO683583	BO683583 AGENCOURT
9	829	29.4	870	5 BO424252	BO424252 AGENCOURT
10	816.4	28.9	850	5 BU146275	BU146275 AGENCOURT
11	806.4	28.6	902	5 BO940423	BO940423 AGENCOURT
12	805	28.5	846	6 CA488057	CA488057 AGENCOURT
13	803.4	28.5	820	5 BX337534	BX337534 BX337534
14	792.6	28.1	877	5 BO221637	BO221637 AGENCOURT
15	792.4	28.1	952	5 BO678130	BO678130 AGENCOURT
16	789.6	28.0	908	5 BO675934	BO675934 AGENCOURT
17	773.8	27.4	917	5 BO683897	BO683897 AGENCOURT
18	772.6	27.4	844	5 BO422555	BO422555 AGENCOURT
19	772	27.4	899	5 BO879177	BO879177 AGENCOURT
20	772	27.4	1118	5 BX440894	BX440894 BX440894
21	768.4	27.2	874	5 BG823347	BG823347 602726742
22	758.6	26.9	926	4 BO677657	BO677657 AGENCOURT
23	758.4	26.9	816	4 BG760961	BG760961 602717657
24	755.2	26.8	884	5 BQ232563	BQ232563 AGENCOURT

25	753.8	26.7	963	5 BO682600	BO682600 AGENCOURT
26	751.6	26.6	1038	4 BM450054	BM450054 AGENCOURT
27	748	26.5	847	4 B1257601	B1257601 602967173
28	745.4	26.4	849	4 BG770331	BG770331 602742359
29	740	26.2	859	4 BO618897	BO618897 602779281
30	739.6	26.2	950	5 BO680533	BO680533 AGENCOURT
31	734	26.0	781	4 B1517279	B1517279 AGENCOURT
32	732.4	25.9	836	2 BE407124	BE407124 601301816
33	732.2	25.9	799	4 BO818657	BO818657 602778844
34	731.8	25.9	799	6 CD620991	CD620991 560680907
35	729.4	25.8	860	5 BO877867	BO877867 AGENCOURT
36	727	25.8	1112	4 BM452153	BM452153 AGENCOURT
37	726.4	25.7	823	2 BF345756	BF345756 602017816
38	723.2	25.6	880	5 BO678891	BO678891 AGENCOURT
39	722.2	25.6	1110	4 BM805296	BM805296 AGENCOURT
40	721	25.5	1048	4 BM452235	BM452235 AGENCOURT
41	717	25.4	826	5 BO883069	BO883069 AGENCOURT
42	709.4	25.1	817	6 CD246163	CD246163 AGENCOURT
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44	703.2	24.9	883	4 B1755503	B1755503 603027361
45	702.2	24.9	709	4 BG761559	BG761559 602718789

## ALIGNMENTS

RESULT 1  
BC013207  
LOCUS  
DEFINITION Homo sapiens G protein-coupled receptor 56, mRNA (CDNA clone IMAGE:4157209).  
ACCESSION BC013207.1 GI:15301450  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bueltow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wooley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shetty, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shetty, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Genome Generation and Initial Analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
JOURNAL MEDLINE  
PUBMED 22388257  
TITLE  
AUTHORS Strausberg, R.  
REFERENCE  
JOURNAL Direct Submission  
Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT  
NIN-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D.



cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louisse, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LML at: <http://image.llnl.gov>  
 Series: IRAK Plate: 12 Row: e Column: 22  
 This clone has the following problem: no 5' EST match.  
 Location/Qualifiers

## FEATURES

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## ORIGIN

Query Match 97.0%; Score 2737.6; DB 3; Length 3835;

Best Local Similarity 99.1%; Pred. No. 0;

Matches 2791; Conservative 0; Mismatches 4; Indels 21; Gaps 3;

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DB 211 CTCACCTCCCGGGTCAAGTATTCATGACCTCAAGCTCCGAGTATGCTGGATTA 270
QY 127 GGTGTGACTTCCAGAGTACTCCGTCCGAGGAAATGACTCCCACTGCTGCTCAG 186
DB 271 GGTGTGACTTCCAGAGTACTCCGTCCGAGGAAATGACTCCCACTGCTGCTCAG 330
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DB 571 CACTTCTGCTCTACTGGAACCGACATGCTGGAGATTACATCTTCTTATGCAAGCT 630
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QY 547 CTGGCTAGAGGAGCCCGCTGTAGGACCTTCTGCACTCTCTGCTGAGGCTTCAGAC 606
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DB 1531 GTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1589
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[illegible]

LOCUS	DEFINITION
AK087268	3295 bp mRNA linear HTC 03-APR-2004
LOCUS	Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone: E030040N19 product: G protein-coupled receptor 56, full insert sequence.
ACCESSION	AK087268
VERSION	AK087268.1 GI:26352409
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komio, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komio, H., Akiyama, J., Nishi, K., Kitsumori, T., Taishiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishide, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Maruyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--364-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
MEDLINE	
PUBMED	
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	
PUBMED	
REFERENCE	6 (bases 1 to 3295)
AUTHORS	Adachi, S., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashimoto, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanakawa, T., Katoh, H., Kojima, Y., Kondo, S., Komio, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Mizuta, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohashi, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akehira, S., Takekoshi, Y., Tanaka, T., Tomaru, A., Toya, T., Yasuniishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Substition
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-72 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome_research@riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,



QY 1652 GGTACAACCTTACCGACTGCTGTGTGAGGTCTTTGGCACTATGTCCTGCTACCTAC 1711  
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 QY 2012 TGGGCTGCGGCGCCCAACCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2071  
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 DB 2144 CCAACCTGCTCCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2202  
 QY 2312 CGAGCCAGGCTCCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2369  
 DB 2203 GTGCTGTGCGCAACCGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2262  
 QY 2370 GAGAGATGAGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2404  
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RESULT 3  
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 DEFINITION Clone CS0D1068YN04 5-PRIME, mRNA sequence.  
 ACCESSION BX381703  
 VERSION BX381703.2 GI:46570764  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 966)  
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 8, 2003 this sequence version replaced gi:30447018.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 8113.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?c=CS0D1068D020P1c=8113.f.  
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ORIGIN  
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 DB 61 GGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120  
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 DB 181 GCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 1569 AGGCTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1628  
 DB 241 AGGCTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 300  
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 DB 301 CTTTCTGAGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 360  
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 DB 361 CACTATATGCTCTGCTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 420  
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 DB 421 TCTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480  
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 DB 481 GCATGAGATCCAGAGGAGGCTCATCTTCTCATCTTCTCATCTTCTCATCTTCTCATCTT 540  
 QY 1869 CAGCTATCATCAACCACTGAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAG 1928  
 DB 541 CAGCTATCATCAACCACTGAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAGGCTGTCAG 600  
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D <sub>b</sub>	721	CTTTGCTTTGACACTCCAGACTTGTCGTCTCTCACTTTTCAGCATCATCACCTCTT	780
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D <sub>b</sub>	781	CCAAGGCTTCTCATCTTCATCTGGATCTGTCCATGCGGCTGCAGGCCCGGGGTGSCC	840
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RESULT 4	BX417949	971 bp	mRNA	linear	EST 01-MAY-2004
LOCUS	BX417949				
DEFINITION	BX417949 Homo sapiens PLACENTA				
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ACCESSION	BX417949				
VERSION	BX417949.2				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1. (bases 1 to 971)				
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On May 13, 2003 this sequence version replaced gi:30637675.				

Genoscope - Centre National de Séquençage  
2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE  
Email: [segrete@genoscope.cns.fr](mailto:segrete@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-0159 (dT) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloneed  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies,  
division of Invitrogen.  
This sequence belongs to sequence cluster 8113.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdata?s=CS00DB014CA01QPlfc-8113.f>.

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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
library was not normalized."

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Query Match	32.0%	Score 904	DB 5	Length 971
Best Local Similarity	96.0%	Pred. No. 1,7e+163		
Matches	893	Conservative	28	Mismatches 9
			Indels	0
			Gaps	0

  

QY	2	GGCACAAGGCTTCGCTCTGTCAACACAGGCTGAGACAGTGTGATCTTGAGCTTCAAC	61
DB	42	GGAGCAGGCTTCGCTCTGTCTGTCAACAGGCTGAGAGTGTGATCTTGAGCTTCAAC	101
QY	62	GTAACCTCCACCTCCCGGATTCAAGTATTCTCATGCTCCAGCTCCAGTACGTGGA	121

Db	102	GTAACTCCAACTCCCGGGTTCAAGTATTTCTATGCTTCAGGCTCCGAGTAGTGGGA	161
Qy	122	TTACAGGTGGTGACTTCCAAAGTGACTCCGTGGAGGAAATGACTTCCCAAGTCGCTGC	181
Db	162	TTACAGGTGGTGACTTCCAAAGTGACTCCGTGGAGGAAATGACTTCCCAAGTCGCTGC	221
Qy	182	TGACAGACGACACTGTCCTGCTGTAAGTCTGCTCTTCCGTGTCAAAGGTGCCACGGACGGG	241
Db	222	TGACAGACGACACTGTCCTGCTGTAAGTCTGCTCTTCCGTGTCAAAGGTGCCACGGACGGG	281
Qy	242	GCCAACAGGAAAGATTTCGCTTTCGACGCCAGGAAACAGACAACAAGACAGCTCC	301
Db	282	GCCAACAGGAAAGATTTCGCTTTCGACGCCAGGAAACAGACAACAAGACAGCTCC	341
Qy	302	ACTACAAACCCACACAGACCTGGGATCTCATTCAGAACTCCGAGAGGACCTTCACAG	361
Db	342	ACTACAAACCCACACAGACCTGGGATCTCATTCAGAACTCCGAGAGGACCTTCACAG	401
Qy	362	TCCATGCCCCCTTTCCTTCGACGCCACCCCTGCTTCCGATCTTCCCTGACCCCAAGGAGC	421
Db	402	TCCATGCCCCCTTTCCTTCGACGCCACCCCTGCTTCCGATCTTCCCTGACCCCAAGGAGC	461
Qy	422	TCTACCACTTTCGCTCTTACTGGAAACCGAATGCTGGGAAATTAATCTTCTTAATGACA	481
Db	462	TCTACCACTTTCGCTCTTACTGGAAACCGAATGCTGGGAAATTAATCTTCTTAATGACA	521
Qy	482	AGCGTAGCTTCTTCTGAGTGAACAACCTCTAGCCTCTCTGCTTCACAGCAGGAGG	541
Db	522	AGCGTAGCTTCTTCTGAGTGAACAACCTCTAGCCTCTCTGCTTCACAGCAGGAGG	581
Qy	542	AGAGCTTGCTCAAGGCCCCCGCTGTTAGCCATTCTGTCACTTCTGTGTGAGGCCCTC	601
Db	582	AGAGCTTGCTCAAGGCCCCCGCTGTTAGCCATTCTGTCACTTCTGTGTGAGGCCCTC	641
Qy	602	AGAACATCAAGCTGCCAGTGGCGGACAGCTTCACTTCTCTCTTCCAGAGTCTTCCACA	661
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Qy	662	CGGCGCTGCACAAATGCTCGGTGGACATGTGCGAGCTCAAAAGGAGCTCAAGCTGTCTCA	721
Db	702	CGGCGCTGCACAAATGCTCGGTGGACATGTGCGAGCTCAAAAGGAGCTCAAGCTGTCTCA	761
Qy	722	GCGAGTTCCTGAAGCATATCCCAAGAGGCTCAAGAGGACCTCGAGCTGCCGCCACAGC	781
Db	762	GCGAGTTCCTGAAGCATATCCCAAGAGGCTCAAGAGGACCTCGAGCTGCCGCCACAGC	821
Qy	782	AGCAGTTGCAAGGCTGGAGTCCGAACCTGACTCTGTGAGATTCAATGGGGGACATGTGT	841
Db	822	AGCAGTTGCAAGGCTGGAGTCCGAACCTGACTCTGTGAGATTCAATGGGGGACATGTGT	881
Qy	842	CCTTGAGAGGAGACCGGATCAAGCCCAAGCGTATGGAAGCTCAGGCCACAGCCGAGCTCC	901
Db	882	CCTTGAGAGGAGACCGGATCAAGCCCAAGCGTATGGAAGCTCAGGCCACAGCCGAGCTCC	941
Qy	902	AGGACCTGCACATCCACTCCGAGCAGAGG	931
Db	942	MRGACCTGCACATCCACTCCGAGCAGAGG	971
RESULT 5			
BX384045			
LOCUS			
DEFINITION			
BX384045 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens			
ACCESSION			
BX384045			
VERSION			
KEYWORDS			
EST.			
SOURCE			
ORGANISM			
Homo sapiens (human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eupheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 941)			



AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 8, 2003 this sequence version replaced gi:30457193.

Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 8113.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?cs=CS0DK003CD02QPI&c=8113.f.

## FEATURES

## source

Location/Qualifiers

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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
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 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 30.2%; Score 852.6; DB 5; Length 941;  
 Best Local Similarity 90.8%; Pred. No. 1.3e-153;  
 Matches 854; Conservative 51; Mismatches 35; Indels 1; Gaps 1;

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QY 122 TTACAGGTGTGACTTCCAGAGTACTCCGTCGAGGAAATGACTCCCAAGTGTGCTGC 181
Db 1 TTACAGGTGTGACTTCCAGAAATGACTCCGTCGAGGAAATGACTCCCAAGTGTGCTGC 60
QY 182 TGCGAGAGCACTGTTCTGCTGAGTGTGCTCTTCTGATCCCAAGTGTGCTGC 241
Db 61 TGCGAGAGCACTGTTCTGCTGAGTGTGCTCTTCTGATCCCAAGTGTGCTGC 120
QY 242 GCCACAGGAGAACTTGTGCTTCTGACGACGAGACCAACACACAGAGAGAGCTTCC 301
Db 121 GCCACAGGAGAACTTGTGCTTCTGACGACGAGACCAACACACAGAGAGAGCTTCC 180
QY 302 ACTACAAACCAACACAGAGCTGCGCATCTCAATGAGAACTCCGAAAGGCGCTCACAG 361
Db 181 ACTACAAACCAACACAGAGCTGCGCATCTCAATGAGAACTCCGAAAGGCGCTCACAG 240
QY 362 TCCAGTCCCTTCTGCTGAGGACCAAGCTTCCGATCTTCCCTGACCCCAAGGCGC 421
Db 241 TCCAGTCCCTTCTGCTGAGGACCAAGCTTCCGATCTTCCCTGACCCCAAGGCGC 300
QY 422 TCTACCACTTCTGCTGACTGAAACCAATGCTGGAAGATTACTTCTCTATGACA 481
Db 301 TCTACCACTTCTGCTGACTGAAACCAATGCTGGAAGATTACTTCTCTATGACA 360
QY 482 AGCGTGAATTTCTGCTGATGACAAAGCTTAAAGCTTCTGCTTCCAGACACAGAGAG 541
Db 361 AGCGTGAATTTCTGCTGATGACAAAGCTTAAAGCTTCTGCTTCCAGACACAGAGAG 420
QY 542 AGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601
Db 421 AGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 602 AGAATCATGAGCTGCGCACTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 661
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Db 541 CGGCGCTGACMAAARCTCGTGAACAMGTGCGARCTCAAAAAGAMCTCCAGTGTCA 600
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Db 661 AACATTTGCAARCTGAGAGTCCAAATGATCTGTGATGATGATGATGATGATGATGATG 720
QY 842 CTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 901
Db 721 CTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 902 AGAATGCAATCTCACTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 961
Db 781 AATATGTCAMACCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 962 TGCTGCTGCTGCAACACTCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Db 841 TGCTGCTGCTGCAACACTCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 1021 AGAATCTCTCTGCTGAGCTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1061
Db 901 AATATCTCTCTGCTGAGCTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 941

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RESULT 6  
 BX339034  
 LOCUS  
 DEFINITION BX339034 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 clone CS0D1066Y14 5-PRIME, mRNA sequence.  
 ACCESSION BX339034  
 VERSION BX339034.2 GI:46281226  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
 AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 2, 2003 this sequence version replaced gi:3043740.

Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 8113.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?cs=CS0D1066Y14&c=8113.f.

## FEATURES

## source

Location/Qualifiers

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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
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## ORIGIN

Query Match 29.9%; Score 844.6; DB 5; Length 981;  
 Best Local Similarity 99.3%; Pred. No. 4.4e-152;  
 Matches 869; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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DB 132 AACCTCACTCCCGGGTTCAGTATCTTCAATCCCTCAAGCTCCCGAGTATGCTGGAT 191
QY 124 ACAGGTGTGATCTTCAAGAGTGACTCGGTGAGAGAAATGATCTCCCGAGTGTGCTGTG 183
DB 192 ACAGGTGTGATCTTCAAGAGTGACTCGGTGAGAGAAATGATCTCCCGAGTGTGCTGTG 251
QY 184 CAGACGACATGTTCTCTGTGAGTCTGTCTTCTGTGCTCAAGGTGCCCAAGGAGGAGC 243
DB 252 CAGACGACATGTTCTCTGTGAGTCTGTCTTCTGTGCTCAAGGTGCCCAAGGAGGAGC 311
QY 244 CACAGGGAAGACTTTCCTTCTGTGAGCAGAGGGAACCAAGACACAGAGAGAGCTCCAC 303
DB 312 CACAGGGAAGACTTTCCTTCTGTGAGCAGAGGGAACCAAGACACAGAGAGAGCTCCAC 371
QY 304 TACAACCCACACACAGAGCTGCGATCTCATGAGAGATCCGAGAGGCTCTCACATC 363
DB 372 TACAACCCACACACAGAGCTGCGATCTCATGAGAGATCCGAGAGGCTCTCACATC 431
QY 364 CATGCCCTTTCCTGAGAGCCCACTGCTGCTCCGATCTTCTGAGCTCCAGGGGCTTC 423
DB 432 CATGCCCTTTCCTGAGAGCCCACTGCTGCTCCGATCTTCTGAGCTCCAGGGGCTTC 491
QY 424 TACCACTTTCCTCTACTGTGAGACGAGATGCTGGAGATTAATCTTCTCATAGGCAAG 483
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DB 672 AACATAGAGCTGAGAGCTGAGAGGCTTCAGCTTCTCTGACAGCTCTCCCAAGCAG 731
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DB 732 GCCGCTCAATGCTGCTGTGAGCACTGTGAGAGCTCAAAAGGAGCTTCAGCTGTGAGC 791
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QY 784 CAGTTCCTGAGAGCTTCCCAAGAGGCTTCAGAGAGGCTTCGAGCTGCCCGCAGAGCAG 843
DB 852 CAGTTCCTGAGAGCTTCCCAAGAGGCTTCAGAGAGGCTTCGAGCTGCCCGCAGAGCAG 910
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DB 911 TTCAGAGAGAGAGCCGAGTCAAGGCCAGGATATGAGAA 944
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RESULT 7
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LOCUS AGENCOURT_7959188 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6110364
DEFINITION 5' mRNA sequence.
ACCESSION BU183659
VERSION BU183659.1 GI:22697643
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  
1 (bases 1 to 932)  
AUTHORS NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LNCM2357 row: 1 column: 13  
High quality sequence stop: 665.  
Location/Qualifiers

## FEATURES

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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 29.9%; Score 843.2; DB 5; Length 932;  
Best Local Similarity 97.4%; Pred. No. 8.3e-152;  
Matches 899; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

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QY 1904 TGTTCCTGTTCAATGAGCCATGCTAGCCACATGATGATGATCAATCTTGGGCTGGCC 1963
DB 132 TGTTCCTGTTCAATGAGCCATGCTAGCCACATGATGATGATCAATCTTGGGCTGGCC 191
QY 1964 CCGACACCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2023
DB 192 CCGACACCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
QY 2024 TGCCCTGGGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2083
DB 252 TGCCCTGGGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 311
QY 2084 ACTTTTCAGATCATCACTCTCTTCCAGAGCTTCCATCTTCAATCTGATCTGATCTGATCA 2143
DB 312 ACTTTTCAGATCATCACTCTCTTCCAGAGCTTCCATCTTCAATCTGATCTGATCTGATCA 371
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DB 372 TGGGCTGAGAGCCCGGGGTGGGCTTCCCTCTGAGAGAGCACTGAGCTGGCAGGC 431
QY 2204 TCCCATGAGCTGGGAGAGCACTTGTCTGAGCTGATCTTGAAGCTTCAGGCCACTGGCC 2263
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[illegible]

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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

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**ORIGIN**

Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

Query Match	29.9%	Score 842.8;	DB 5;	Length 965;
Best Local Similarity	94.9%	Pred. NO. 9.9e-152;		
Matches 914; Conservative	0;	Mismatches 43;	Indels 6;	Gaps 4;

[illegible]







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583 TGGCCCTGACAAGGCTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642  
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703 AGGCTTTTGGACCTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762  
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VERSION CA488057.1 GI:24948944  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1 (bases 1 to 846)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
AUTHORS Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-remail.nih.gov  
Tissue Procurement: Kristi A. Eglund, Ira Pastan  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA sequencing by: Agencourt Bioscience Corporation  
DNA distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:

http://image.liml.gov  
Plate: LIML4278 row: e column: 09  
High quality sequence stop: 694.  
Location/Qualifiers  
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Directionally cloned. Priming method: oligo-dT. Average  
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Kristi A. Eglund, James J. Vincent, Robert Strausberg,  
Bungkok Lee & Ira Pastan. Discovery of new breast  
cancer genes encoding membrane and secreted proteins.  
Manuscript submitted."

ORIGIN  
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Best Local Similarity 97.7%; Pred. No. 1.9e-144; Indels 19; Gaps 2;  
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1675 GTGAGAGTCTTTGACCTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1734  
463 GTGAGAGTCTTTGACCTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522  
1735 GGGTTCCTCCATCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1793  
523 GGGTTCCTCCATCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582  
1794 CATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853  
583 CATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642  
1854 CCGGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1913

Db 643 CCGGAGCTCCCTGTGAGTACATCAACCTGGGCTCTTTCAGCCGTGGTGTCTT 702  
Qy 1914 CAACATGGGATGAGTACGACCATGATGATGAGATCTGGGCTGCGCCGACACCA 1973  
Db 703 CAACATGGGATGAGTACGACCATGATGATGAGATCTGGGCTGCGCCGACACCA 762  
Qy 1974 AAAGTGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2033  
Db 763 AAAGTGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 822  
Qy 2034 CTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2057  
Db 823 CTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846

RESULT 13  
BX37534 820 bp mRNA linear EST 07-APR-2004  
LOCUS BX37534 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0D1043YG13 5-PRIME, mRNA sequence.  
ACCESSION BX37534 GI:46273908  
VERSION BX37534.2  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 2, 2003 this sequence version replaced gi:30339619.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
8113.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS0D1043AD07QPI&c=8113.f.  
FEATURES  
source  
1..820  
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/mol\_type="mRNA"  
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/clone="CS0D1043YG13"  
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/note="1st strand cDNA was primed with a NotI-oligo (dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  
ORIGIN  
Query Match 28.5%; Score 803.4; DB 5; Length 820;  
Best Local Similarity 99.8%; Pred No. 3.8e-144; Indels 1; Gaps 1;  
Matches 815; Conservative 0; Mismatches 1;  
Qy 1472 AACCTGGGACTACATCAATGATGATGATGATGATGATGATGATGATGAT 1531  
Db 5 AACCTGGGACTACATCAATGATGATGATGATGATGATGATGATGATGAT 64  
Qy 1532 ACAGAGCTTCTGTCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1591  
Db 65 ACAGAGCTTCTGTCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 124  
Qy 1592 CCAGTGCATCTTCTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1651  
Db 125 CCAGTGCATCTTCTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184

Qy 1652 GGTACACCTTACACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1711  
Db 185 GGTACACCTTACACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244  
Qy 1712 TCAAGTGAAGCCCAATGGGCTGGGCTTCCCATCTTTCTGCTGCTGCTGCTGCT 1771  
Db 245 TCAAGTGAAGCCCAATGGGCTGGGCTTCCCATCTTTCTGCTGCTGCTGCTGCT 304  
Qy 1772 TGAATGTGACAACTATGAGCCCATCATCTTGGCTGCTGCTGCTGCTGCTGCT 1831  
Db 305 TGAATGTGACAACTATGAGCCCATCATCTTGGCTGCTGCTGCTGCTGCTGCT 364  
Qy 1832 TCTACCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1891  
Db 365 TCTACCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424  
Qy 1892 TCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1951  
Db 425 TCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484  
Qy 1952 TGGGCTGCGGCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 2011  
Db 485 TGGGCTGCGGCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 544  
Qy 2012 TGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2071  
Db 545 TGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604  
Qy 2072 TTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2131  
Db 605 TTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 664  
Qy 2132 GGTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2191  
Db 665 GGTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723  
Qy 2192 ACTGCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2251  
Db 724 ACTGCGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783  
Qy 2252 GCCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2288  
Db 784 GCCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820

RESULT 14  
BQ221637 877 bp mRNA linear EST 02-MAY-2002  
LOCUS BQ221637  
DEFINITION AGENCOURT 7592842 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6050253  
5', mRNA sequence.  
ACCESSION BQ221637  
VERSION BQ221637.1 GI:20403037  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS NIH-MGC http://mgi.mgi.nhl.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC/DCMP/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L14M13502 row: C column: 22  
High quality sequence stop: 608.

FEATURES  
Source

Location/Qualifiers  
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/issue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_72"  
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI,  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

Query Match 28.1%; Score 792.6; DB 5; Length 877;  
Best Local Similarity 96.2%; Pred. No. 4.5e-142;  
Matches 844; Conservative 0; Mismatches 29; Indels 4; Gaps 3;

1795 ATCATCTTGGCTGGCATAGAGACTCCAGAGGGCGTCACTACCCCTTCATGCTGATC 1854  
1 ATCATCTTGGCTGGCATAGAGACTCCAGAGGGCGTCACTACCCCTTCATGCTGATC 60  
1855 CGGAGCTCCCTGTGAGCTATACCAACCACTGGGCTCTTCAGGCTGATGTTCTGTTTC 1914  
61 CGGAGCTCCCTGTGAGCTATACCAACCACTGGGCTCTTCAGGCTGATGTTCTGTTTC 120  
1915 AACATGGGCATGCTAGCCACCACTGGTGTGATCTCTGCGGCTGCGCCCAACCCAA 1974  
121 AACATGGGCATGCTAGCCACCACTGGTGTGATCTCTGCGGCTGCGCCCAACCCAA 180  
1975 AAGTGTGACATGCTGACACTGCTGGGCGTCACTGGCTGCTGGCTGCGCGGAGCC 2034  
181 AAGTGTGACATGCTGACACTGCTGGGCGTCACTGGCTGCTGGCTGCGCGGAGCC 240  
2035 TTGATCTTCTTCTCTTCTTCTTCTGGAACCTTCAGCTTGTGCTCTTACCTTTTACG 2094  
241 TTGATCTTCTTCTCTTCTTCTTCTGGAACCTTCAGCTTGTGCTCTTACCTTTTACG 300  
2095 ATCATACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2154  
301 ATCATACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 360  
2155 GCCCGGGGTGGCCCTCCCTCTGTAAGAGCAACATGAGCTGGCGAGGCTCCCATACG 2214  
361 GCCCGGGGTGGCCCTCCCTCTGTAAGAGCAACATGAGCTGGCGAGGCTCCCATACG 420  
2215 TCGGGCAGACCTGTGTCAAGCGCATCTAGAGCTTCAGCCCACTGCCCATGTGTAAG 2274  
421 TCGGGCAGACCTGTGTGTCAAGCGCATCTAGAGCTTCAGCCCACTGCCCATGTGTAAG 480  
2275 CAGAGATGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2334  
481 CAGAGATGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
2335 AGTCAGCGCAGACTTTGAAAAGCCCAAGCAACATGAGAGAGAGGCGGTCATGCTG 2394  
541 AGTCAGCGCAGACTTTGAAAAGCCCAAGCAACATGAGAGAGAGGCGGTCATGCTG 600  
2395 GACGAGCTCCCGGGGCTGGGCTTTTGAATTGGCTTGGGGACTTCTGGCTCTACCTCA 2454  
601 GACGAGCTCCCGGGGCTGGGCTTTTGAATTGGCTTGGGGACTTCTGGCTCTACCTCA 658  
2455 GCTCCCAAGGAGCTCAGAAAGTGGCGGCGCATGCTAGGAGTACGTCCTCCCAATCTGT 2514  
659 GCTCCCAAGGAGCTCAGAAAGTGGCGGCGCATGCTAGGAGTACGTCCTCCCAATCTGT 718  
2515 CCACACCGAGCTGAGAGGCTGTCTCTTCAACCCCTGGGCGAG-CTCATATGCTG 2573  
719 CCACACCGAGCTGAGAGGCTGTCTCTTCAACCCCTGGGCGAG-CTCATATGCTG 778  
2574 GGGGCGAGGCGCTT-GGATCTTGAAGGCTGTGAGCATCTCTTATCTGTGCGGCTGCGG 2632

DB 779 GGGGCGAGGCGCTTGGATCTTGAAGGCTGTGAGACATCCCTAAATCTGTGCGCTGCG 838  
QY 2633 GACGAAATGTGTGCTCCAGTGTGCTGTCTCTGCTG 2669  
DB 839 GACGAAATGTGTGCTCCAGTGTGCTGTCTCTGCTG 875

RESULT 15  
BO678130 952 bp mRNA linear EST 15-JUN-2002  
LOCUS  
DEFINITION  
AGENCOURT 8419783 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6273707  
5', mRNA sequence.  
BO678130  
ACCESSION  
VERSION  
BO678130.1 GI:21790809  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 952)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
AUTHORS  
CONTACT: Robert Strausberg, Ph.D.  
Email: [cgapds-remail.nih.gov](mailto:cgapds-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
Plate: LICM2454 row: b column: 12  
High quality sequence stop: 551.

FEATURES  
Source

Location/Qualifiers  
1. 952  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6273707"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_112"  
/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 28.1%; Score 792.4; DB 5; Length 952;  
Best Local Similarity 94.4%; Pred. No. 4.9e-142;  
Matches 898; Conservative 0; Mismatches 42; Indels 11; Gaps 7;

1772 TGAATGTGAGCAACTATGAGCCCATCATCTTGGCTGTGATAGACTCAGAGGGCGTCA 1831  
1 TGAATGTGAGCAACTATGAGCCCATCATCTTGGCTGTGATAGACTCAGAGGGCGTCA 60  
1832 TCTACCTTCAATGTGTGATTCGGAGCTCCCTGTGTGAGCTATCACTCAACCTGGGCG 1891  
61 TCTACCTTCAATGTGTGATTCGGAGCTCCCTGTGTGAGCTATCACTCAACCTGGGCG 120  
1892 TCTTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1951  
121 TCTTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180  
1952 TCGGCTGCGCCCAACCCAAAGTGTGATGATGTCTGACATGCTGAGCTGCGGCTCAGCC 2011  
181 TCGGCTGCGCCCAACCCAAAGTGTGATGATGTCTGACATGCTGAGCTGCGGCTCAGCC 240



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 22:57:42 ; Search time 1773 Seconds

(without alignments)  
586.787 Million cell updates/sec

Title: US-10-073-054-14

Perfect score: 22  
Sequence: 1 ttcgagatcctcgcagcagc 22

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364484945 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

Database :

GenBank1:  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	95.5	372	6	BD076161 5' EST of
2	21	95.5	423	6	BD081288 Sequence
3	21	95.5	423	6	CQ115834 Sequence
4	21	95.5	423	6	CQ154602 Sequence
5	21	95.5	423	6	CQ187133 Sequence
6	21	95.5	423	6	CQ237857 Sequence
7	21	95.5	423	6	CQ275479 Sequence
8	21	95.5	423	6	CQ312440 Sequence
9	21	95.5	423	6	CQ349899 Sequence
10	21	95.5	493	6	CQ407379 Sequence
11	21	95.5	582	6	CQ072149 Sequence
12	21	95.5	582	6	CQ102837 Sequence
13	21	95.5	582	6	CQ141717 Sequence
14	21	95.5	582	6	CQ177316 Sequence
15	21	95.5	582	6	CQ225007 Sequence
16	21	95.5	582	6	CQ263027 Sequence
17	21	95.5	582	6	CQ300060 Sequence
18	21	95.5	582	6	CQ337293 Sequence
19	21	95.5	739	6	CQ780635 Sequence

20	21	95.5	739	6	CQ782177 Sequence
21	21	95.5	739	6	BD125344 Primer to
22	21	95.5	739	6	BD126886 Primer to
23	21	95.5	745	6	AX136607 Sequence
24	21	95.5	745	6	BD123847 Sequence
25	21	95.5	2061	6	CQ755181 Sequence
26	21	95.5	2082	6	AX029423 Sequence
27	21	95.5	2082	6	AX429262 Sequence
28	21	95.5	2082	6	BD062445 Novel rec
29	21	95.5	2082	9	BT007311 Homo sapi
30	21	95.5	2082	12	BT009896 Synthetic
31	21	95.5	2821	6	CQ715549 Sequence
32	21	95.5	2822	6	AX298003 Sequence
33	21	95.5	2822	6	AX549232 Sequence
34	21	95.5	2822	9	AF106858 Homo sapi
35	21	95.5	2834	6	AX029424 Sequence
36	21	95.5	2834	6	BD062446 Novel rec
37	21	95.5	3564	6	AX965647 Sequence
38	21	95.5	3586	6	AX061726 Sequence
39	21	95.5	3702	9	BC008770 Homo sapi
40	21	95.5	3748	6	CQ783397 Sequence
41	21	95.5	3748	6	BD127626 Primer to
42	21	95.5	3748	6	AK075270 Homo sapi
43	21	95.5	3774	6	AX136371 Sequence
44	21	95.5	3774	6	BD123638 Secretory
45	21	95.5	3774	9	AK075555 Homo sapi
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47	21	95.5	3819	6	AX358880 Sequence
48	21	95.5	3819	6	AX362373 Sequence
49	21	95.5	3819	6	AX454506 Sequence
50	21	95.5	3819	6	AX464272 Sequence
51	21	95.5	3819	6	AX490984 Sequence
52	21	95.5	3819	6	AY358400 Homo sapi
53	21	95.5	3845	6	AY358400 Homo sapi
54	21	95.5	3845	9	HS011001 Novel gene
55	21	95.5	3902	6	CQ412946 Sequence
56	21	95.5	13695	6	AX646713 Sequence
57	21	95.5	13695	9	AB065909 Homo sapi
58	21	95.5	152156	9	AC018552 Homo sapi
59	20	90.9	480	6	CQ394642 Sequence
60	20	90.9	480	6	CQ400995 Sequence
61	19.4	88.2	301589	1	AB017312 Desulfotol
62	18.8	85.5	1715	8	AF054902 Continuation (23 o
63	18.4	83.6	110000	1	AP005260 Oryza sat
64	18.4	83.6	135315	8	AP005189 Oryza sat
65	18.4	83.6	141702	8	AP005189 Oryza sat
66	17.8	80.9	1997	3	AJ748329 Heliothis
67	17.8	80.9	2725	8	AK110297 Oryza sat
68	17.8	80.9	6120	1	AY303700 Bifidobac
69	17.8	80.9	10058	1	AB001752 Thermotog
70	17.8	80.9	35964	3	CEB0365 Caenorhabdi
71	17.8	80.9	110000	8	CR380947-1 Continuation (2 of
72	17.8	80.9	188050	1	AL646072 Ralstonia
73	17.8	80.9	300330	3	CNS06C8G Chromosom
74	17.8	80.9	300330	1	AP005222 Oryza sat
75	17.4	79.1	1064	8	AK062198 Oryza sat
76	17.4	79.1	2053	6	AK067958 Oryza sat
77	17.4	79.1	2058	6	AK067958 Oryza sat
78	17.4	79.1	2118	6	AX659812 Sequence
79	17.4	79.1	2167	6	AX660346 Sequence
80	17.4	79.1	2301	6	AX660320 Sequence
81	17.4	79.1	2627	8	AK067757 Oryza sat
82	17.4	79.1	2640	8	AK067757 Oryza sat
83	17.4	79.1	2668	8	AK067726 Oryza sat
84	17.4	79.1	2783	8	AF404820 Neurospor
85	17.4	79.1	8623	8	CNS0584Q Oryza sat
86	17.4	79.1	12797	1	AE007229 Sinothiza
87	17.4	79.1	83015	8	CNS08C8T Oryza sat
88	17.4	79.1	100773	8	AP466201 Sorghum b
89	17.4	79.1	104849	8	CNS08C8T Oryza sat
90	17.4	79.1	152828	8	AC133859 Oryza sat
91	17.4	79.1	152828	8	AC133859 Oryza sat
92	17.2	78.2	1661	8	TRRNVALIS Tuberc cf. r



93	17.2	78.2	1714	8	TE18SR	X98089 T. excavatum	166	16.8	76.4	137040	8	AP005806	AP005806 Oryza sat
94	17.2	78.2	1714	8	AP054904	AP054904 Choicowic	167	16.8	76.4	137218	2	OSJ000037	AL606617 Oryza sat
95	17.2	78.2	2000	6	AX461405	AX461405 Sequence	168	16.8	76.4	137263	2	AC068740	AC068740 Homo sapi
96	17.2	78.2	3254	1	AY048197	AY048197 Frankia s	169	16.8	76.4	139968	8	AP004161	AP004161 Oryza sat
97	17.2	78.2	3619	9	BC010674	BC010674 Homo sapi	170	16.8	76.4	141674	2	AC080046	AC080046 Homo sapi
98	17.2	78.2	3641	6	CO716253	CO716253 Sequence	171	16.8	76.4	141782	2	AP005582	AP005582 Oryza sat
99	17.2	78.2	3643	9	H0MPTVPH	M68941 Human prote	172	16.8	76.4	143400	8	AC134927	AC134927 Oryza sat
100	17.2	78.2	4208	9	HSW08076	BS648614 Homo sapi	173	16.8	76.4	143717	2	AC134927	AC134927 Oryza sat
101	17.2	78.2	31045	3	CEK08825	AC104658 Homo sapi	174	16.8	76.4	143966	2	AC135920	AC135920 Oryza sat
102	17.2	78.2	39565	3	CEK08825	Z81668 Caenorhabd	175	16.8	76.4	145254	2	AC114681	AC114681 Oryza sat
103	17.2	78.2	45319	1	PF1297913	AJ297913 Plasmid p	176	16.8	76.4	145818	8	AP003746	AP003746 Oryza sat
104	17.2	78.2	45675	8	AF039047	AF039047 Caenorhab	177	16.8	76.4	147836	8	AP003983	AP003983 Oryza sat
105	17.2	78.2	80472	8	AC007945	AC007945 Genomic s	178	16.8	76.4	151533	8	AC090873	AC090873 Oryza sat
106	17.2	78.2	87849	3	AC084453	AC084453 Caenorhab	179	16.8	76.4	151841	9	AC105233	AC105233 Homo sapi
107	17.2	78.2	99923	8	FS08	AC005990 Arabidops	180	16.8	76.4	152599	9	AC092745	AC092745 Oryza sat
108	17.2	78.2	110000	1	BSX50851_42	Continuation (43 o	181	16.8	76.4	155702	8	OSJ000137	OSJ000137 Oryza sat
109	17.2	78.2	110000	2	AP006501_00	Continuation (43 o	182	16.8	76.4	155847	8	AC092766	AC092766 Oryza sat
110	17.2	78.2	139055	2	AC015719	AP006501 Cyanidior	183	16.8	76.4	158173	8	AC092778	AC092778 Oryza sat
111	17.2	78.2	158450	10	AC068911	AC015719 Homo sapi	184	16.8	76.4	163639	9	AC097493	AC097493 Oryza sat
112	17.2	78.2	163615	10	AC068913	AC068911 Mus muscu	185	16.8	76.4	163733	9	AC127526	AC127526 Oryza sat
113	17.2	78.2	164262	2	AC147723	AC147723 Pongo pyg	186	16.8	76.4	164155	9	AC000385	AC000385 Homo sapi
114	17.2	78.2	172487	10	AL954375	AL954375 Mouse DNA	187	16.8	76.4	165187	5	AC147883	AC147883 Xenopus t
115	17.2	78.2	176578	2	AC041008	AC041008 Homo sapi	188	16.8	76.4	165987	5	AC147883	AC147883 Pan trogl
116	17.2	78.2	215416	10	AC129537	AC129537 Mus muscu	189	16.8	76.4	167576	2	AC147297	AC147297 Homo sapi
117	17.2	78.2	228267	2	AC096381	AC096381 Rattus no	190	16.8	76.4	171832	9	AC079942	AC079942 Homo sapi
118	17.2	78.2	233417	10	AL844416	AL844416 Mouse DNA	191	16.8	76.4	171862	8	AC130732	AC130732 Oryza sat
119	17.2	78.2	239381	2	AC111319	AC111319 Rattus no	192	16.8	76.4	172647	8	AC130732	AC130732 Oryza sat
120	17.2	78.2	243968	2	AC130131	AC130131 Rattus no	193	16.8	76.4	174171	9	AC068587	AC068587 Homo sapi
121	17.2	78.2	262936	2	AC121467	AC121467 Rattus no	194	16.8	76.4	174826	2	AC116562	AC116562 Homo sapi
122	17.2	78.2	280422	2	AC112901	AC112901 Rattus no	195	16.8	76.4	177203	2	AC135424	AC135424 Oryza sat
123	17.2	78.2	300298	8	AE016881	AE016881 Eremothec	196	16.8	76.4	177574	8	AC073648	AC073648 Homo sapi
124	17.2	78.2	300298	8	AE016788	AE016788 Pseudomon	197	16.8	76.4	180659	9	AC130349	AC130349 Homo sapi
125	17.2	78.2	302550	1	BE294137	BE294137 Pirellula	198	16.8	76.4	189043	2	AC130349	AC130349 Homo sapi
126	17.2	78.2	302988	1	AE017176	AE017176 Porphyrom	199	16.8	76.4	189043	2	AC130349	AC130349 Homo sapi
127	17.2	77.3	4529	3	AE017293	U729316 Caedra segyp	200	16.8	76.4	206192	2	AC034259	AC034259 Oryza sat
128	17.2	77.3	27248	3	CEK08824	Z68316 Caenorhabd	201	16.8	76.4	224391	2	AC126644	AC126644 Rattus no
129	16.8	76.4	334	9	HSW08081	Z68315 H. sapiens t	202	16.8	76.4	224395	2	AC097413	AC097413 Homo sapi
130	16.8	76.4	548	11	BA185446	BA185446 sqm14814	203	16.8	76.4	226899	2	AC097413	AC097413 Homo sapi
131	16.8	76.4	1361	8	AA581481	AJ581481 Apeyrgill	204	16.8	76.4	292100	9	AF228730	AF228730 Homo sapi
132	16.8	76.4	16053	8	AK103360	AJ103360 Oryza sat	205	16.8	76.4	295854	9	AF228730	AF228730 Homo sapi
133	16.8	76.4	2653	5	DRE245964	AJ245964 Danio rer	206	16.8	76.4	305584	2	AE017250	AE017250 Treponema
134	16.8	76.4	2702	9	AK091914	AK091914 Homo sapi	207	16.8	76.4	302085	1	AE017054	AE017054 Oryza sat
135	16.8	76.4	3193	9	CCU06928	U06928 Caulobacter	208	16.8	76.4	302085	2	AC006879	AC006879 Caenorhab
136	16.8	76.4	6515	9	AB007953	AB007953 Homo sapi	209	16.8	76.4	305518	2	AE016920	AE016920 Rattus no
137	16.8	76.4	10475	8	YL16754	AJ006754 Yarrowia	210	16.8	76.4	305584	2	AC095802	AC095802 Oryza sat
138	16.8	76.4	10482	8	AE010498	AE010498 Pseudocete	211	16.8	76.4	316339	2	AF102407	AF102407 Coutoubea
139	16.8	76.4	10792	1	AE011585	AE011585 Leptospir	212	16.4	74.5	410	8	AF105082	AF105082 Triclicum
140	16.8	76.4	11250	1	AE011947	AE011947 Xanthomon	213	16.4	74.5	418	8	AF105082	AF105082 Triclicum
141	16.8	76.4	11835	1	AE007258	AB007258 Sinorhizo	214	16.4	74.5	427	8	AF105082	AF105082 Triclicum
142	16.8	76.4	12680	1	AE005970	AE005970 Caulobact	215	16.4	74.5	630	11	BV033294	BV033294 Homo sapi
143	16.8	76.4	14857	8	AC145385	AC145385 Oryza sat	216	16.4	74.5	656	8	AY083951	AY083951 Arabidops
144	16.8	76.4	30352	3	U28412	U28412 Caenorhabd	217	16.4	74.5	749	5	CR353298	CR353298 Gallus ga
145	16.8	76.4	38102	3	CBR814K24	AC084504 Caenorhabd	218	16.4	74.5	3768	14	BSU35768	BSU35768 Barley strit
146	16.8	76.4	38102	8	AP006750	AP006750 Oryza sat	219	16.4	74.5	3783	14	BSU35768	BSU35768 Barley strit
147	16.8	76.4	42380	8	AP005922	AP005922 Oryza sat	220	16.4	74.5	3787	14	PAU81259	PAU81259 Pseudomonas
148	16.8	76.4	58408	1	AE017300_3	Continuation (4 of	221	16.4	74.5	7295	1	AE005928	AE005928 Pseudomonas
149	16.8	76.4	61588	10	AL611970	Continuation (4 of	222	16.4	74.5	10813	1	AE005928	AE005928 Pseudomonas
150	16.8	76.4	62726	2	AC084090	AC084090 Homo sapi	223	16.4	74.5	11415	1	AE004889	AE004889 Pseudomonas
151	16.8	76.4	66521	2	AC137893	AC137893 Homo sapi	224	16.4	74.5	12746	1	AE001016	AE001016 Archaeogl
152	16.8	76.4	67261	2	AC103715	AC103715 Homo sapi	225	16.4	74.5	12746	1	AE001016	AE001016 Archaeogl
153	16.8	76.4	73103	2	AC090106	AC090106 Homo sapi	226	16.4	74.5	12746	1	AE001016	AE001016 Archaeogl
154	16.8	76.4	92171	9	AC004924	AC004924 Homo sapi	227	16.4	74.5	67943	3	AF125952	AF125952 Caenorhab
155	16.8	76.4	97556	9	AC079781	AC079781 Homo sapi	228	16.4	74.5	74328	8	FI3K23	FI3K23 Arabidops
156	16.8	76.4	110000	2	AC032450_4	Continuation (5 of	229	16.4	74.5	80117	8	AB025628	AB025628 Arabidops
157	16.8	76.4	110000	8	CR382129_14	Continuation (15 o	230	16.4	74.5	84487	8	OSJ000006	OSJ000006 Homo sapi
158	16.8	76.4	110000	8	CR382132_28	Continuation (29 o	231	16.4	74.5	85513	2	AC125064	AC125064 Lotus cor
159	16.8	76.4	117046	8	AC135600	AC135600 Oryza sat	232	16.4	74.5	97807	2	AP006696	AP006696 Arabidops
160	16.8	76.4	118553	8	AP005865	AP005865 Oryza sat	233	16.4	74.5	110000	1	AB046436	AB046436 Arabidops
161	16.8	76.4	120139	8	AP003498	AP003498 Homo sapi	234	16.4	74.5	110000	8	LMF1CHR16_09	LMF1CHR16_09 Continuation (14 o
162	16.8	76.4	121340	8	AP003498	AP003498 Homo sapi	235	16.4	74.5	110000	8	CR380955_01	CR380955_01 Continuation (10 o
163	16.8	76.4	122130	2	AC005326	AC005326 Homo sapi	236	16.4	74.5	110000	8	CR382132_06	CR382132_06 Continuation (7 of
164	16.8	76.4	129043	2	AC128143	AC128143 Rattus no	237	16.4	74.5	110000	8	CR382132_06	CR382132_06 Continuation (7 of
165	16.8	76.4	132268	8	AC099733	AC099733 Oryza sat	238	16.4	74.5	111551	9	AL360178	AL360178 Human DNA

C 239	16.4	74.5	116952	8	OSJN00010	AL606453	Oryza sat	C 312	16.2	73.6	399	8	AF102466	AF102466	Orphium f
C 240	16.4	74.5	138989	8	AC063973	AC063973	Genomic S	C 313	16.2	73.6	399	8	AF102499	AF102499	Xestoea 1
C 241	16.4	74.5	144885	10	AL731766	AL731766	Mouse DNA	C 314	16.2	73.6	399	8	AF402222	AF402222	Centauriu
C 242	16.4	74.5	157947	8	OSJN00260	AL731614	Oryza sat	C 315	16.2	73.6	399	8	AF402231	AF402231	Centauriu
C 243	16.4	74.5	157947	8	OSJN00260	AL731614	Oryza sat	C 316	16.2	73.6	399	8	AF15678	AF15678	Centauriu
C 244	16.4	74.5	165339	3	CEY57A10A	AL117195	Caenorhab	C 317	16.2	73.6	399	8	AF15679	AF15679	Centauriu
C 245	16.4	74.5	180716	2	AC118169	AC118169	Rattus no	C 318	16.2	73.6	400	8	AF102402	AF102402	Centauriu
C 246	16.4	74.5	184810	10	AC090869	AC090869	Mus Muscu	C 319	16.2	73.6	400	8	AF156148	AF156148	Centauriu
C 247	16.4	74.5	225739	2	AC115646	AC115646	Rattus no	C 320	16.2	73.6	400	8	AF156681	AF156681	Centauriu
C 248	16.4	74.5	233364	2	BM571949	BM571949	Danio rer	C 321	16.2	73.6	400	8	AF15682	AF15682	Centauriu
C 249	16.4	74.5	236184	2	AC134125	AC134125	Rattus no	C 322	16.2	73.6	400	8	AF15683	AF15683	Centauriu
C 250	16.4	74.5	250918	2	AC106517	AC106517	Rattus no	C 323	16.2	73.6	400	8	AF15684	AF15684	Centauriu
C 251	16.4	74.5	252127	10	AC133576	AC133576	Mus muscu	C 324	16.2	73.6	401	8	CB4490197	CB4490197	Centauriu
C 252	16.4	74.5	260361	2	AC101347	AC101347	Rattus no	C 325	16.2	73.6	401	8	CL1490199	CL1490199	Centauriu
C 253	16.4	74.5	261844	2	AC101331	AC101331	Rattus no	C 326	16.2	73.6	401	8	AF402200	AF402200	Centauriu
C 254	16.4	74.5	264755	2	AC137353	AC137353	Rattus no	C 327	16.2	73.6	401	8	AF402211	AF402211	Centauriu
C 255	16.4	74.5	277000	1	SC0939109	AL939109	Streptomy	C 328	16.2	73.6	401	8	AF102476	AF102476	Centauriu
C 256	16.4	74.5	299925	1	AP005048	AP005048	Streptomy	C 329	16.2	73.6	402	8	AF402199	AF402199	Centauriu
C 257	16.4	74.5	300129	1	AE017309	AE017309	Desulfovy	C 330	16.2	73.6	402	8	AF402205	AF402205	Centauriu
C 258	16.4	74.5	349761	1	BM482646	BM482646	Bdellovib	C 331	16.2	73.6	402	8	AF402209	AF402209	Centauriu
C 259	16.2	73.6	155	8	AY201009	AY201009	Arabidops	C 332	16.2	73.6	402	8	AF402215	AF402215	Centauriu
C 260	16.2	73.6	158	8	CO434993	CO434993	Sequence	C 333	16.2	73.6	402	8	AF402216	AF402216	Centauriu
C 261	16.2	73.6	201	11	BY202831	BY202831	sqm21002	C 334	16.2	73.6	402	8	AF402217	AF402217	Centauriu
C 262	16.2	73.6	211	10	MUSPTKV	L25762	Mus muscu	C 335	16.2	73.6	402	8	AF402217	AF402217	Centauriu
C 263	16.2	73.6	242	5	AY266813	AY266813	Gadus mor	C 336	16.2	73.6	402	8	AF402218	AF402218	Centauriu
C 264	16.2	73.6	378	8	AY251749	AY251749	Centauriu	C 337	16.2	73.6	402	8	AF402219	AF402219	Centauriu
C 265	16.2	73.6	378	8	AY251750	AY251750	Centauriu	C 338	16.2	73.6	402	8	AF402248	AF402248	Centauriu
C 266	16.2	73.6	393	8	BE4490200	AL490200	Eustoma e	C 339	16.2	73.6	402	8	AF402250	AF402250	Centauriu
C 267	16.2	73.6	393	8	AY251741	AY251741	Ixanthus	C 340	16.2	73.6	402	8	AF402252	AF402252	Centauriu
C 268	16.2	73.6	394	8	AF102390	AF102390	Canescora	C 341	16.2	73.6	402	8	AF402253	AF402253	Centauriu
C 269	16.2	73.6	395	8	AF102416	AF102416	Eustoma r	C 342	16.2	73.6	402	8	AY251733	AY251733	Centauriu
C 270	16.2	73.6	396	8	AY251752	AY251752	Eustoma e	C 343	16.2	73.6	402	8	AY251738	AY251738	Centauriu
C 271	16.2	73.6	396	8	AY155685	AY155685	Schenkia	C 344	16.2	73.6	402	8	AY251746	AY251746	Centauriu
C 272	16.2	73.6	396	8	AY155686	AY155686	Schenkia	C 345	16.2	73.6	402	8	AY251747	AY251747	Centauriu
C 273	16.2	73.6	396	8	AY155687	AY155687	Zeltnera	C 346	16.2	73.6	403	8	CL4490198	CL4490198	Centauriu
C 274	16.2	73.6	396	8	AY155689	AY155689	Zeltnera	C 347	16.2	73.6	403	8	AF102477	AF102477	Centauriu
C 275	16.2	73.6	396	8	AY155690	AY155690	Zeltnera	C 348	16.2	73.6	403	8	AF102477	AF102477	Centauriu
C 276	16.2	73.6	396	8	AY155691	AY155691	Zeltnera	C 349	16.2	73.6	403	8	AF102477	AF102477	Centauriu
C 277	16.2	73.6	396	8	AY155692	AY155692	Zeltnera	C 350	16.2	73.6	404	8	AF402242	AF402242	Centauriu
C 278	16.2	73.6	396	8	AY155693	AY155693	Zeltnera	C 351	16.2	73.6	404	8	AF402242	AF402242	Centauriu
C 279	16.2	73.6	396	8	AY155694	AY155694	Zeltnera	C 352	16.2	73.6	404	8	AF402242	AF402242	Centauriu
C 280	16.2	73.6	396	8	AY155695	AY155695	Zeltnera	C 353	16.2	73.6	404	8	AF402244	AF402244	Centauriu
C 281	16.2	73.6	396	8	AY155696	AY155696	Zeltnera	C 354	16.2	73.6	405	8	AF402244	AF402244	Centauriu
C 282	16.2	73.6	397	8	AF402228	AF402228	Centauriu	C 355	16.2	73.6	405	8	AF402244	AF402244	Centauriu
C 283	16.2	73.6	397	8	AY155680	AY155680	Gyrandra	C 356	16.2	73.6	406	8	AF402249	AF402249	Centauriu
C 284	16.2	73.6	397	8	AY155688	AY155688	Zeltnera	C 357	16.2	73.6	406	8	AF402251	AF402251	Centauriu
C 285	16.2	73.6	398	8	OPR490244	AF102394	Orphium f	C 358	16.2	73.6	407	8	MP4490241	MP4490241	Centauriu
C 286	16.2	73.6	398	8	AF102394	AF102394	Centauriu	C 359	16.2	73.6	407	8	AF402240	AF402240	Centauriu
C 287	16.2	73.6	398	8	AF402293	AF402293	Centauriu	C 360	16.2	73.6	407	8	AY251729	AY251729	Centauriu
C 288	16.2	73.6	398	8	AF402206	AF402206	Centauriu	C 361	16.2	73.6	407	8	AY251731	AY251731	Centauriu
C 289	16.2	73.6	398	8	AF402210	AF402210	Centauriu	C 362	16.2	73.6	410	8	AY251732	AY251732	Centauriu
C 290	16.2	73.6	398	8	AF402214	AF402214	Centauriu	C 363	16.2	73.6	410	8	AY255694	AY255694	Centauriu
C 291	16.2	73.6	398	8	AF402220	AF402220	Centauriu	C 364	16.2	73.6	410	8	AY255694	AY255694	Centauriu
C 292	16.2	73.6	398	8	AF402221	AF402221	Centauriu	C 365	16.2	73.6	413	8	AF402204	AF402204	Centauriu
C 293	16.2	73.6	398	8	AF402223	AF402223	Centauriu	C 366	16.2	73.6	413	8	AF402243	AF402243	Centauriu
C 294	16.2	73.6	398	8	AF402224	AF402224	Centauriu	C 367	16.2	73.6	413	8	AF402245	AF402245	Centauriu
C 295	16.2	73.6	398	8	AF402225	AF402225	Centauriu	C 368	16.2	73.6	413	8	AF402246	AF402246	Centauriu
C 296	16.2	73.6	398	8	AF402226	AF402226	Centauriu	C 369	16.2	73.6	413	8	AF402247	AF402247	Centauriu
C 297	16.2	73.6	398	8	AF402229	AF402229	Centauriu	C 370	16.2	73.6	413	8	AY251730	AY251730	Centauriu
C 298	16.2	73.6	398	8	AF402230	AF402230	Centauriu	C 371	16.2	73.6	413	8	AY251735	AY251735	Centauriu
C 299	16.2	73.6	398	8	AF402232	AF402232	Centauriu	C 372	16.2	73.6	413	8	AY251737	AY251737	Centauriu
C 300	16.2	73.6	398	8	AF402233	AF402233	Centauriu	C 373	16.2	73.6	416	8	AY255693	AY255693	Centauriu
C 301	16.2	73.6	398	8	AF402234	AF402234	Centauriu	C 374	16.2	73.6	417	5	AF402201	AF402201	Centauriu
C 302	16.2	73.6	398	8	AF402235	AF402235	Centauriu	C 375	16.2	73.6	417	5	AF402201	AF402201	Centauriu
C 303	16.2	73.6	398	8	AF402237	AF402237	Centauriu	C 376	16.2	73.6	417	5	AF402201	AF402201	Centauriu
C 304	16.2	73.6	398	8	AF402238	AF402238	Centauriu	C 377	16.2	73.6	417	5	AF402201	AF402201	Centauriu
C 305	16.2	73.6	398	8	AF402239	AF402239	Centauriu	C 378	16.2	73.6	418	8	NCND52781	NCND52781	Centauriu
C 306	16.2	73.6	398	8	AF402253	AF402253	Centauriu	C 379	16.2	73.6	756	3	AY226070	AY226070	Centauriu
C 307	16.2	73.6	399	8	CAL490191	CAJ490191	Canescora	C 380	16.2	73.6	1161	5	AB091097	AB091097	Centauriu
C 308	16.2	73.6	399	8	CAN490192	CAJ490192	Canescora	C 381	16.2	73.6	1185	3	AY334315	AY334315	Centauriu
C 309	16.2	73.6	399	8	CD1490193	AF102389	Canescora	C 382	16.2	73.6	1206	1	AY337171	AY337171	Centauriu
C 310	16.2	73.6	399	8	AF102389	AF102389	Canescora	C 383	16.2	73.6	1320	3	S78531	S78531	Centauriu
C 311	16.2	73.6	399	8	AF102415	AF102415	Eustoma e	C 384	16.2	73.6	1453	6	CO579240	CO579240	Sequence

385	16.2	73.6	1496	8	AK069460	AK069460 Oryza sat	C 458	16.2	73.6	21576	1	AE004128	AE004128 Vibrio ch
386	16.2	73.6	1510	8	AK072478	AK072478 Oryza sat	C 459	16.2	73.6	22188	6	CG612407	CG612407 Sequence
387	16.2	73.6	1580	10	MUSLGBB	M32018 Mouse LysoB	C 460	16.2	73.6	22653	3	DROMHC	M61229 D.melanog
388	16.2	73.6	1681	6	AX877772	AX877772 Sequence	C 461	16.2	73.6	23360	3	DHMHHC	X77570 D.hydrei mmH
389	16.2	73.6	1881	6	BD156840	BD156840 Primer to	C 462	16.2	73.6	27056	8	CRU303349	AJ303349 Capsella
390	16.2	73.6	1881	9	AK001895	AK001895 Homo sapi	C 463	16.2	73.6	29001	2	AC019796	AC019796 Drosophila
391	16.2	73.6	1944	8	AY250704	AY250704 Glycine m	C 464	16.2	73.6	31495	1	BU033883	BU033883 Brachyrob
392	16.2	73.6	1994	8	NMCWACP	X83578 N.crassa ml	C 465	16.2	73.6	32012	3	CER1166	250795 Caenorhabd
393	16.2	73.6	2001	6	AR442653	AR442653 Sequence	C 466	16.2	73.6	33553	2	AC020055	AC020055 Drosophila
394	16.2	73.6	2010	6	AR137624	AR137624 Sequence	C 467	16.2	73.6	37357	2	CET06C12	281116 Caenorhabd
395	16.2	73.6	2010	6	AX019702	AX019702 Sequence	C 468	16.2	73.6	38790	2	AC014072	AC014072 Drosophila
396	16.2	73.6	2124	9	HSMB03820	AL834512 Homo sapi	C 469	16.2	73.6	42934	8	SPBC947	AL021837 S.pombe c
397	16.2	73.6	2139	1	AB036425	AB036425 Rhodobact	C 470	16.2	73.6	50089	3	AC005641	AC005641 Drosophila
398	16.2	73.6	2179	3	AK067821	AK067821 Oryza sat	C 471	16.2	73.6	54657	2	ROX53676	AC017422 Drosophila
399	16.2	73.6	2197	8	AY05511	AY05511 Mesocyclo	C 472	16.2	73.6	57405	2	AC017422	AC019798 Drosophila
400	16.2	73.6	2232	6	CO805550	CO805550 Sequence	C 473	16.2	73.6	60144	2	AC019798	AC019919 Drosophila
401	16.2	73.6	2233	8	AY142646	AY142646 Arabidops	C 474	16.2	73.6	61550	2	ATAC011698	AC015199 Arabidops
402	16.2	73.6	2248	6	AR148582	AR148582 Sequence	C 475	16.2	73.6	63654	8	ATAC011698	AC005519 Drosophila
403	16.2	73.6	2498	6	AR349059	AR349059 Sequence	C 476	16.2	73.6	68379	3	AC005519	AP006383 Lotus cor
404	16.2	73.6	2594	9	AF071542	AF071542 Homo sapi	C 477	16.2	73.6	73179	8	AP006383	EX842598 Neurospor
405	16.2	73.6	2636	6	AX001289	AX001289 Sequence	C 478	16.2	73.6	73541	8	AP000417	AP000417 Arabidops
406	16.2	73.6	2636	6	AX001289	AX001289 Sequence	C 479	16.2	73.6	73977	8	AP000417	AC019835 Drosophila
407	16.2	73.6	2636	6	AX154554	AX154554 Sequence	C 480	16.2	73.6	85560	2	AC019835	AC017116 Homo sapi
408	16.2	73.6	2636	6	AF030698	AF030698 Homo sapi	C 481	16.2	73.6	86801	8	AC007120	AC007120 Genomic s
409	16.2	73.6	2660	6	CQ729594	CQ729594 Sequence	C 482	16.2	73.6	89690	2	AL335552	Continuation (4 of
410	16.2	73.6	2661	6	BD171301	BD171301 Gene enco	C 483	16.2	73.6	90157	9	AL335552	Continuation (4 of
411	16.2	73.6	2661	9	AF069493	AF069493 Homo sapi	C 484	16.2	73.6	90157	9	AC004935	Continuation (7 of
412	16.2	73.6	2718	1	AF079406	AF079406 Vibrio ch	C 485	16.2	73.6	102389	3	AC004935	Continuation (14 of
413	16.2	73.6	2836	3	AY069416	AY069416 Drosophila	C 486	16.2	73.6	103428	8	ATP3A4	Continuation (18 of
414	16.2	73.6	2870	3	AK116450	AK116450 Clona int	C 487	16.2	73.6	108158	2	AE017283	Continuation (8 of
415	16.2	73.6	3230	10	HHER2	M96653 Mus muscicul	C 488	16.2	73.6	110000	1	AE017283	Continuation (6 of
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420	16.2	73.6	3999	6	AX001328	AX001328 Sequence	C 493	16.2	73.6	118948	8	AP004326	Continuation (14 of
421	16.2	73.6	4445	5	XLXFIN	XK0601 Xenopus lae	C 494	16.2	73.6	121088	2	AP004326	Continuation (14 of
422	16.2	73.6	4782	6	CQ579239	CQ579239 Sequence	C 495	16.2	73.6	126020	3	AP004326	Continuation (14 of
423	16.2	73.6	4858	6	CQ597380	CQ597380 Sequence	C 496	16.2	73.6	132708	8	AP004326	Continuation (14 of
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436	16.2	73.6	7475	6	AX001323	AX001323 Sequence							
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452	16.2	73.6	12497	1	AE014868	AE014868 Streptoco							
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454	16.2	73.6	13406	1	AE007887	AE007887 Agrobacte							
455	16.2	73.6	13595	3	CG613655	CG613655 Sequence							
456	16.2	73.6	14759	6	CEK12012	Z49069 Caenorhabd							
457	16.2	73.6	19177	6	CG000275	CG000275 Sequence							

## ALIGNMENTS

RESULT 1	BD076161/c	372 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD076161/c	5' EST of tissue-nonspecific secretory protein.			
DEFINITION	BD076161	5' EST of tissue-nonspecific secretory protein.			
ACCESSION	BD076161.1	GI:2621764			
VERSION	BD076161.1	GI:2621764			
KEYWORDS	JP 2001512011-A/109.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Edwards, J.B.D.M., Ductert, A. and Lacroix, B.				
AUTHORS	Edwards, J.B.D.M., Ductert, A. and Lacroix, B.				
TITLE	5' EST of tissue-nonspecific secretory protein				
JOURNAL	Patent: JP 2001512011-A 109 21-AUG-2001;				
COMMENT	OS Homo sapiens (human)				
	PN JP 2001512011-A/109				
	PD 21-AUG-2001				
	PF 31-JUL-1998 JP 2000505289				
	PR 01-AUG-1997 US 08/905135				
	PI JEAN BAPTISTE DUMAS-MILNE EDWARDS, AYMERIC DUCTERT, BRUNO PI				
	LACROIX				
	PC C12N15/09, C12N15/09, C07K14/47, C1201/68, C12N15/00, C12N15/00 CC				
	blastn				

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CC identity 94  
CC region 322. .372  
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CC identity 97  
CC region 261. .306  
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FH Key Location/Qualifiers  
FH misc feature 147. .264  
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FT sig\_peptide 184. .258.  
Location/Qualifiers  
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## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 372;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 369 TTCGAGTTCGATGAGAT 349

RESULT 2  
C0081288 423 bp DNA linear PAT 20-JAN-2004  
LOCUS C0081288  
DEFINITION Sequence 17088 from Patent WO0157278.  
ACCESSION C0081288  
VERSION C0081288.1 GI:41051157  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human hela cells or other human  
cervical epithelial cells  
JOURNAL Patent: WO 0157278-A 17088 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 122 TTCGAGTTCGATGAGAT 102

RESULT 3  
LOCUS CQ115834 423 bp DNA linear PAT 21-JAN-2004  
DEFINITION Sequence 24693 from Patent WO0157272.  
ACCESSION CQ115834  
VERSION CQ115834.1 GI:41085704  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human placenta  
JOURNAL Patent: WO 0157272-A 24693 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
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## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 423;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCGAGTTCGATGAGAT 21  
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Db 122 TTCGAGTTCGATGAGAT 102

RESULT 4  
CQ154602 423 bp DNA linear PAT 21-JAN-2004  
LOCUS CQ154602  
DEFINITION Sequence 24624 from Patent WO0157276.  
ACCESSION CQ154602  
VERSION CQ154602.1 GI:41161954  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157276-A 24624 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCGAGTTCGATGAGAT 21  
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Db 122 TTCGAGTCTCGATCGAGAT 102

RESULT 5			
LOCUS	CO187133/c		
DEFINITION	Sequence 18529 from Patent WO0157274.	423 bp	DNA
ACCESSION	CO187133		linear
VERSION	CO187133.1	GI:41182145	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		

**REFERENCE**  
**AUTHORS** 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
**TITLE** Human genome-derived single exon nucleic acid probes useful for  
**JOURNAL** analysis of gene expression in human heart  
Patent: WO 0157274-A 18529 09-AUG-2001;  
Acemica, Inc. (US)

**ORIGIN**

Query Match	95.5%	Score 21	DB 6	Length 423
Best Local Similarity	100.0%	Pred. No. 40		
Matches 21	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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QY      1 TTGGAGTTCTCGATGAGAT 21
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Db     122 TTCGAGTTCGATGAGAT 102
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RESULT 6	CQ237857/c	423 bp	DNA	linear	PAT 21-JAN-200
LOCUS	CQ237857				
DEFINITION	Sequence 24696 from Patent WO0157273.				
ACCESSION	CQ237857				
VERSION	CQ237857.1	GI:4122137			
KEYWORDS					
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				

REFERENCE  
AUTHORS  
TITLE

1  
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

ORIGIN	EVALU 0.00e+00
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Query Match	95.5%	Score 21	DB 6	Length 423
Best local similarity	100.0%	Pred. No. 40		
Matches	21	Conservative	0	Mismatches 0; Indels 0; Gaps 0.
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Db	122	TTGGAGTTCGATGGAGAT	102	

RESULT	7			
LOCUS	CQ275479/c			
DEFINITION	CQ275479	423 bp	DNA	linear
ACCESSION	Sequence 23740 from Patent WO0157277.			PAT 23-JAN-2001
VERSION	CQ275479			
KEYWORDS	CQ275479.1 GI:41248083			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Euteleostomi; Vertebrata; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Rutimorpha; Merizoa;			

RESULT 7	LOCUS	SEQUENCE	SIZE	ORIGIN
CO275479/c	CO275479	423 bp	DNA	linear
ACCION	Sequence	23740	from Patent WO0157277.	
VERSION	CO275479			
KEYWORDS	CO275479.1	GI:41248083		
SOURCE				
ORGANISM				
	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE				
AUTHORS	1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.			
TITLE	Human genome-derived single exon nucleic acid probes useful for			
JOURNAL	analyses of gene expression in human fetal liver			
	Patent: WO 0157277-A 23740 09-AUG-2001;			
FEATURES	Acemica, Inc. (US)			
Source	location/Qualifiers			
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REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1	Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.	Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver	Patent: WO 0157277-A 23740 09-AUG-2001;	source Aeomica, loc. (US) location/Qualifiers 1..423 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="MAP TO AC018552.2-EXPRESSED IN FETAL LIVER, SIGNAL = 5.8-SWISSPROT HIT: P28984, EVALUATE 3.70e-01-NT HIT: AJ011001.1, EVALUATE 0.00e+00-EST_HUMAN HIT: AL046540.1, EVALUATE 0.00e+00"

**ORIGIN**

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Db      122 TTCGAGTTCGATGGAGAT  102

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LOCUS	CQ312440				
DEFINITION	Sequence 23545 from Patent WO0186003.				
ACCESSION	CQ312440				
VERSION	CQ312440.1				
KEYWORDS	GI:41273017				
SOURCE	Homo sapiens (human)				

REFERENCE AUTHORS TITLE JOURNAL
Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung Patent: WO 0186003-A 23545 15-NOV-2001; Aeomica, Inc. (US)

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 40;  
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Db 122 TTGGAGTTCGATGAGAT 102

RESULT 9  
LOCUS CQ349899/c 423 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 23993 from Patent WO0157275.  
ACCESSION CQ349899  
VERSION CQ349899.1 GI:41238970  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W., and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human brain  
JOURNAL Patent: WO 0157275-A 23993 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source location/Qualifiers  
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AJ011001.1, EVALUATE 0.00e+00-EST\_HUMAN HIT: AL046540.1,  
EVALUATE 0.00e+00"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 423;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 122 TTGGAGTTCGATGAGAT 102

RESULT 10  
LOCUS CQ407379/c 493 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 14450 from Patent WO0170979.  
ACCESSION CQ407379  
VERSION CQ407379.1 GI:41315160  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Lee, J. and Lillie, J.  
TITLE Genes, compositions, kits, and method for identification,  
assessment, prevention, and therapy of ovarian cancer  
JOURNAL Patent: WO 0170979-A 14450 27-SEP-2001;  
Millennium Pharmaceutical, Inc. (US)  
FEATURES  
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RESULT 11  
LOCUS CQ072149/c 582 bp DNA linear PAT 20-JAN-2004  
DEFINITION Sequence 7949 from Patent WO0157278.  
ACCESSION CQ072149  
VERSION CQ072149.1 GI:41042018  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W., and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human hela cells or other human  
cervical epithelial cells  
JOURNAL Patent: WO 0157278-A 7949 09-AUG-2001;  
Aeomica, Inc. (US)  
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Db 227 TTGGAGTTCGATGAGAT 207

RESULT 12  
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DEFINITION Sequence 11696 from Patent WO0157272.  
ACCESSION CQ102837  
VERSION CQ102837.1 GI:41071863  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W., and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
analysis of gene expression in human placenta  
JOURNAL Patent: WO 0157272-A 11696 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN PLACENTA, SIGNAL =  
7.2"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;



Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 13  
CQ141717/c 582 bp DNA linear PAT 21-JAN-2004  
LOCUS Sequence 11739 from Patent WO0157276.  
DEFINITION CQ141717  
ACCESSION CQ141717.1 GI:41099089  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow  
JOURNAL Patent: WO 0157276-A 11739 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..582  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN BONE MARROW, SIGNAL = 5.4"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 14  
CQ177316/c 582 bp DNA linear PAT 21-JAN-2004  
LOCUS Sequence 8712 from Patent WO0157274.  
DEFINITION CQ177316  
ACCESSION CQ177316.1 GI:41172055  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart  
JOURNAL Patent: WO 0157274-A 8712 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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/note="MAP TO AC018552.2-EXPRESSED IN HEART, SIGNAL = 4.7"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 227 TTGGAGTTCTCGATGAGAT 207

DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 15  
CQ225007/c 582 bp DNA linear PAT 21-JAN-2004  
LOCUS Sequence 11846 from Patent WO0157273.  
DEFINITION CQ225007  
ACCESSION CQ225007.1 GI:41207461  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine  
Patent: WO 0157273-A 11846 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..582  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN ADULT LIVER, SIGNAL = 5.7"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 16  
CQ263027 582 bp DNA linear PAT 23-JAN-2004  
LOCUS Sequence 11288 from Patent WO0157277.  
DEFINITION CQ263027  
ACCESSION CQ263027.1 GI:41235507  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver  
JOURNAL Patent: WO 0157277-A 11288 09-AUG-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..582  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN FETAL LIVER, SIGNAL = 5.8"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 17  
LOCUS CQ300060/c 582 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 11165 from Patent WO0186003.  
ACCESSION CQ300060  
VERSION CQ300060.1 GI:41260637  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
JOURNAL analysis of gene expression in human lung  
Patent: WO 0186003-A 1165 15-NOV-2001;  
Aecomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. 582  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN LUNG, SIGNAL = 6.5"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 18  
LOCUS CQ337293/c 582 bp DNA linear PAT 23-JAN-2004  
DEFINITION Sequence 11387 from Patent WO0157275.  
ACCESSION CQ337293  
VERSION CQ337293.1 GI:41286364  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.  
TITLE Human genome-derived single exon nucleic acid probes useful for  
JOURNAL analysis of gene expression in human brain  
Patent: WO 0157275-A 11387 09-AUG-2001;  
Aecomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. 582  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="MAP TO AC018552.2-EXPRESSED IN BRAIN, SIGNAL = 7.8"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 582;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 227 TTGGAGTTCTCGATGAGAT 207

RESULT 19  
LOCUS CQ780635/c 739 bp DNA linear PAT 17-MAR-2004  
DEFINITION Sequence 775 from Patent EP1396543.  
ACCESSION CQ780635  
VERSION CQ780635.1 GI:45536707  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
Koga, H.

TITLE Primers for synthesizing full length cDNA clones and their use  
JOURNAL Research Association for Biotechnology (JP)  
Patent: EP 1396543-A 775 10-MAR-2004;  
Location/Qualifiers  
1. 739  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 739;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 430 TTGGAGTTCTCGATGAGAT 410

RESULT 20  
LOCUS CQ782177/c 739 bp DNA linear PAT 17-MAR-2004  
DEFINITION Sequence 2317 from Patent EP1396543.  
ACCESSION CQ782177  
VERSION CQ782177.1 GI:45538233  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
Koga, H.  
TITLE Primers for synthesizing full length cDNA clones and their use  
JOURNAL Patent: EP 1396543-A 2317 10-MAR-2004;  
Research Association for Biotechnology (JP)  
Location/Qualifiers  
1. 739  
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/db\_xref="taxon:9606"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 739;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 430 TTGGAGTTCTCGATGAGAT 410

RESULT 21  
LOCUS BD125344/c 739 bp DNA linear PAT 18-SEP-2002  
BD125344

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DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD125344
VERSION BD125344.1 GI:23220289
KEYWORDS JP 2002017375-A/775.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 739)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 775 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/775
PD 22-JAN-2002
PP 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
PC 10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT source 1..739
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/location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 95.5%; Score 21; DB 6; Length 739;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21
DB 430 TTCGAGTTCTCGATGAGAT 410

RESULT 22
BD126886/c 739 bp DNA linear PAT 18-SEP-2002
LOCUS BD126886
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD126886
VERSION BD126886.1 GI:23221831
KEYWORDS JP 2002017375-A/2317.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 739)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2317 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2317
PD 22-JAN-2002
PP 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI

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SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
PC 10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT source 1..739
/organism="Homo sapiens (human)"
/location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
location/Qualifiers
1..739
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 95.5%; Score 21; DB 6; Length 739;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21
DB 430 TTCGAGTTCTCGATGAGAT 410

RESULT 23
AX136607/c 745 bp DNA linear PAT 30-MAY-2001
LOCUS AX136607
DEFINITION Sequence 529 from Patent EP1067182.
ACCESSION AX136607
VERSION AX136607.1 GI:14273011
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 745)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
Secretory protein or membrane protein
Patent: EP 1067182-A 529 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
FT source 1..745
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 95.5%; Score 21; DB 6; Length 745;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21
DB 453 TTCGAGTTCTCGATGAGAT 433

RESULT 24
BD123847/c 745 bp DNA linear PAT 18-SEP-2002
LOCUS BD123847
DEFINITION Secretory protein or membrane protein.
ACCESSION BD123847
VERSION BD123847.1 GI:23218792
KEYWORDS JP 2002017376-A/356.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 745)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.

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**TITLE** Secretory protein or membrane protein  
**JOURNAL** Patent : JP 2002017376-A 356 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
**COMMENT**  
 OS Homo sapiens (human)  
 PN JP 2002017376-A/356  
 PD 22-JAN-2002  
 PF 07-JUL-2000 JP 2000253173  
 PI TOSHIO OTA, TAKAO ISOGLI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU  
 PI SUGIYAMA,  
 PI KOJI HAYASHI  
 PC  
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
 10,  
 PC C12P21/02, C12Q1/68//C12P21/08, C12N15/00, C12N5/00 CC  
 Secretory protein or membrane protein  
**FT** Key Location/Qualifiers  
**FT** source 1..745  
**FEATURES** Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="Genomic DNA"  
 /db\_xref="taxon:9606"

**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 TTCCGAGTTCTCGATGAGAT 21  
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 453 TTCCGAGTTCTCGATGAGAT 433

**RESULT 25**  
**LOCUS** CQ755181 2061 bp DNA linear PAT 01-MAR-2004  
**DEFINITION** Sequence 74 from Patent EP1375515.  
**ACCESSION** CQ755181  
**VERSION** CQ755181.1 GI:44846115  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
 1 Fukushima, D., Shibayama, S. and Tada, H.  
 Polypeptide, cDNA encoding the same, and use thereof  
 Patent: EP 1375515-A 74 02-JAN-2004;  
 ONO PHARMACEUTICAL CO., LTD. (JP)  
**FEATURES** Location/Qualifiers  
 source 1..2061  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 2061;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 TTCCGAGTTCTCGATGAGAT 21  
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 186 TTCCGAGTTCTCGATGAGAT 166

**RESULT 26**  
**LOCUS** AX029423 2082 bp DNA linear PAT 16-SEP-2000  
**DEFINITION** Sequence 3 from Patent WO9915551.  
**ACCESSION** AX029423  
**VERSION** AX029423.1 GI:10190216  
**KEYWORDS**

**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
 1 Herzog, H.  
 Novel receptor  
 Patent: WO 9915551-A 3 01-APR-1999;  
 GARVAN INST MED RES (AU); HERZOG HERBERT (AU)  
**FEATURES** Location/Qualifiers  
 source 1..2082  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 2082;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 TTCCGAGTTCTCGATGAGAT 21  
 |||||  
 186 TTCCGAGTTCTCGATGAGAT 166

**RESULT 27**  
**LOCUS** AX429262 2082 bp DNA linear PAT 02-JUL-2002  
**DEFINITION** Sequence 1 from Patent WO0234781.  
**ACCESSION** AX429262  
**VERSION** AX429262.1 GI:21540569  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
 1 Berger, C., Van Rander, J. and Tulp, M.T.M.  
 Human G-protein coupled diadenosine tetraphosphate receptor (AP4AR)  
 Patent: WO 0234781-A 1 02-MAY-2002;  
 SOLVAY PHARM GMBH (DE)  
**FEATURES** Location/Qualifiers  
 source 1..2082  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 2082;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 TTCCGAGTTCTCGATGAGAT 21  
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 186 TTCCGAGTTCTCGATGAGAT 166

**RESULT 28**  
**LOCUS** BD062445 2082 bp DNA linear PAT 27-AUG-2002  
**DEFINITION** Novel receptor.  
**ACCESSION** BD062445  
**VERSION** BD062445.1 GI:22608048  
**KEYWORDS** JP 2001513653-A/1.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE**  
 1 Herzog, H.  
 Novel receptor  
 Patent: JP 2001513653-A 1 04-SEP-2001;  
 GARVAN INSTITUTE OF MEDICAL RESEARCH

COMMENT OS Homo sapiens (human)  
 PN JP 2001513653-A/1  
 PD 04-SEP-2001  
 PR 24-SEP-1998 JP 1999518348  
 PF 24-SEP-1997 AU PO 9386  
 PI HERBERT HERZOG  
 PC C07K7/06, C07K14/705, C07K16/28, C12N15/12, C12N5/10, C12P21/02, PC  
 A01K67/027,  
 PC GOIN33/68, C07H21/04  
 CC  
 FH Key Location/Qualifiers  
 1. .2082  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

FEATURES  
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 1. .2082  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="BD Creator (TM) CDS library derived from MGC  
 collection"  
 /lab\_host="DH5alpha T1 resistant"  
 /note="Vector: pDNR-Dual"  
 1. .2082

CDS

Query Match 95.5%; Score 21; DB 6; Length 2082;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
 |||||  
 186 TTCCGAGTTCTCGATGAGAT 166

Db

RESULT 29  
 BT007311/c 2082 bp mRNA linear PRI 13-MAY-2003  
 LOCUS Homo sapiens G protein-coupled receptor 56 mRNA, complete cds.  
 DEFINITION BT007311  
 ACCESSION BT007311.1 GI:30583460  
 VERSION FLI CDNA.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 2082)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Phelan,M. and Farmer,A.  
 Cloning of human full-length CDS in BD Creator (TM) System Donor  
 vector

TITLE Unpublished  
 2 (bases 1 to 2082)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Phelan,M. and Farmer,A.  
 Direct Submission  
 Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow  
 Circle, Palo Alto, CA 94303, USA  
 This CDS clone is a part of a collection of human full length  
 expression clones generated by BD Biosciences Clontech and the  
 Harvard Institute of Proteomics. Each CDS has been cloned in two  
 forms: with and without stop-codon (to allow fusion with C-terminal  
 tag). The CDS has been directionally cloned using BP In-Fusion (TM)  
 cloning system between the SalI and HindIII sites of the pDNR-DUAL  
 vector. Additional sequences in the clone: 'ACC' after SalI site  
 and before 'ATG' to provide Kozak consensus sequence; 'GG' after  
 last codon and before HindIII site to maintain reading frame.  
 Clone distribution: http://bioinfo.clontech.com/orfclones.  
 Location/Qualifiers  
 1. .2082  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="BD Creator (TM) CDS library derived from MGC  
 collection"  
 /lab\_host="DH5alpha T1 resistant"  
 /note="Vector: pDNR-Dual"  
 1. .2082

/codon\_start=1  
 /product="G protein-coupled receptor 56"  
 /protein\_id="AAP35975.1"  
 /db\_xref="GI:30583461"  
 /translation="MTPOSILQTLTFLSLFLVQAGRGHREDPRFCGQRNQTGRS  
 SLHYKPTPLRLISENSEKALIVHAPFPAHPSARSPDPRLGYHFLWNRHAGLH  
 LLYGKRDPLSLRSKASLSCFOHSESLAQGPPLATSVSWSPNLSLPSASPTES  
 PHSPPRTAHNNSVSMCEKRLDCLISGLKHPKRSRRPSAASQGLQSLSKLT  
 VFMGDMVSEEDRINATYKQLOPTGDDDLHNSQBERQSIIMEYSVLPTPTLOR  
 TGRSGSEAKRLLLDVSSQALFQDNSSHVJAEKVLGIVONTKANTLTPVLTPO  
 HOLQPKNTVLQCFWVEDPTLSPGHMSAGCEVTRRTQSCFNHLYTFAVLMVS  
 VEYDAVHKHYLSLSYGCVSNAICLVTAIYICSRVPLPCRKRPRDYTIKVHMLL  
 LAVFLDPTSLSEPEVPAALGSEACGSAIPLHFSILTCLSMWEGEYLYRAVEVF  
 GYVYPCYLIKLSMGWGPPIPLVTIYALVDVNDYGPILIAVHRTPGCVIYPSMCWID  
 SLVSYITNGLGSLVFLPNNMALTATVQILRLRPRTKRSHTLTIGLSLVGLPWA  
 LIFFSASGTFQLVLYLPSITTSFGFLFTYWMRLQARGPSPDKNSDARLP  
 ISSGSTSSRI"

ORIGIN

Query Match 95.5%; Score 21; DB 9; Length 2082;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
 |||||  
 186 TTCCGAGTTCTCGATGAGAT 166

Db

RESULT 30  
 BT009896/c 2082 bp mRNA linear SYN 02-AUG-2003  
 LOCUS Synthetic construct Homo sapiens G protein-coupled receptor 56  
 DEFINITION BT009896  
 ACCESSION BT009896.1 GI:32880134  
 VERSION FLI CDNA.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 2082)  
 Kainine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
 Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
 Phelan,M. and Farmer,A.  
 Direct Submission  
 Submitted (17-JUL-2003) BD Biosciences Clontech, 1020 East Meadow  
 Circle, Palo Alto, California 94303, USA  
 This CDS clone is a part of a collection of human full length  
 expression clones generated by BD Biosciences Clontech and the  
 Harvard Institute of Proteomics. Each CDS has been cloned in two  
 forms: with and without stop-codon (to allow fusion with C-terminal  
 tag). The CDS has been directionally cloned using BP In-Fusion (TM)  
 cloning system between the SalI and HindIII sites of the  
 pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after  
 SalI site and before 'ATG' to provide Kozak consensus sequence;  
 'GG' after last codon and before HindIII site to maintain reading  
 frame.  
 Clone distribution: http://bioinfo.clontech.com/orfclones.  
 Location/Qualifiers  
 1. .2082  
 /organism="Synthetic construct"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:32630"  
 /clone\_lib="BD Creator (TM) CDS library derived from MGC  
 collection"  
 /lab\_host="DH5alpha T1 resistant"  
 /note="Vector: pDNR-Dual"  
 1. .2082

CDS

1..>2082  
/note="Mutations: 2081:stop->L"  
/codon\_start=1  
/transl\_table=1  
/product="g protein-coupled receptor 56"  
/protein\_id="AAP8898.1"  
/db\_xref="GI:32880135"  
/translation="MTPOSILQTTLLFLILSLFLVGAHGRGHREDFRFCQOROTHS  
SLHKTPDRLRISTENSEEALTAHAPPAARSPDPDGLVHPCLYMRHGRHL  
LVYGRDPLSDKASLLCFQHSESLAQGPLATSTTSMWSRONISLPSAASPTSS  
FSPBPTAAHNAVDMCELRDLQLSLQFLHPOKASRPSAARPSQQLQSESLTIS  
VRFWGDMVSPFEDRIINAVMKLQPLAQDLHHSROEQLMEYSVLLPRLFOR  
TKRSGAEKELLVDFSSQALFQDKNSHVLGKGVIGIVONTNANLTPVVLTEQ  
HQLQPKVTLQCVWVEDPTLSPGHMSAGCEYRRETQSCFNHLTPYAVLVSS  
VEDNAVHRYVLSLISVGCIVSALACIVTIAVLCRYPPLPCRPRDYTLKXNNIL  
LAVPLDTSFLISRPVALTGSBACRAAIFLHBSLITCLSMGLEGVNLYRIVVEF  
GTVPVGLIKLSANGWGPFLVTLVVALVDNDNGPITLAVHRTPEGVITYSMCIIR  
SLVSYITNLGLFSLVFLPNNMAMLTMMVQILRLRPHTKMSHVLTLLSLVLGLPMA  
LIFPSFAGTFQLVLYLFLSIITTSFQGLIFITWMSMLQARGGSPPLKNSNSDARLP  
ISSGSTSSRL"

ORIGIN

Query Match 95.5%; Score 21; DB 12; Length 2082;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 186 TTGGAGTTCTCGATGAGAT 166  
|||||

RESULT 31  
LOCUS CQ715549 2821 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 1483 from Patent WO02068579.  
ACCESSION CQ715549  
VERSION CQ715549.1 GI:42276406  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 1483 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES  
source 1..2821  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2821;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 348 TTGGAGTTCTCGATGAGAT 328  
|||||

RESULT 32  
LOCUS AX298003 2822 bp DNA linear PAT 26-NOV-2001  
DEFINITION Sequence 1 from Patent WO0183558.  
ACCESSION AX298003  
VERSION AX298003.1 GI:11728089  
KEYWORDS  
SOURCE Homo sapiens (human)

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 348 TTGGAGTTCTCGATGAGAT 328  
|||||

RESULT 33  
LOCUS AX549232 2822 bp DNA linear PAT 26-NOV-2002  
DEFINITION Sequence 517 from Patent WO02061087.  
ACCESSION AX549232  
VERSION AX549232.1 GI:25813927  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Burner, G.C., Roush, C.L. and Brown, J.P.  
TITLE Antigenic peptides, such as for G protein-coupled receptors  
(GPCRs), antibodies thereto, and systems for identifying such  
antigenic peptides  
JOURNAL Patent: WO 02061087-A 517 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)  
FEATURES  
source 1..2822  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
Db 348 TTGGAGTTCTCGATGAGAT 328  
|||||

RESULT 34  
LOCUS AF106858 2822 bp mRNA linear PRI 17-MAY-1999  
DEFINITION Homo sapiens G-protein-coupled receptor (GPR56) mRNA, complete cds.  
ACCESSION AF106858  
VERSION AF106858.1 GI:4836764  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Liu, M., Parker, R.M., Darby, K., Byre, H.J., Copeland, N.G.,  
Crawford, J., Gilbert, D.J., Sutherland, G.R., Jenkins, N.A. and



TITLE Herzog, H.  
GPR56, a novel secretin-like human G-protein-coupled receptor gene  
JOURNAL Genomics 55 (3), 296-305 (1999)  
MEDLINE 99168899

REFERENCE 10049584  
2 (bases 1 to 2822)  
AUTHORS Herzog, H.

TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1999) Neurobiology, Garvan Institute, 384  
Victoria St., Sydney, NSW 2010, Australia

FEATURES  
source Location/Qualifiers

1..2822  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/map="q31"  
1..2822  
/gene="GPR56"  
163..2244  
/gene="GPR56"  
/note="SLR32"  
/codon\_start=1  
/product="G-protein-coupled receptor"  
/protein\_id="AB030545.1"  
/db\_xref="GI:4836765"

/translation="MTPOGLQTTLLFLSLFLVQAGRGHREDFRFGSQQRNQHRS  
SLHYKTPDLRISENESEALTVHAPPAHPASRFPDPPRGLYHPCLYMNRAGRLH  
LHYKRPDLISKASLCEFOEESLAQPPPLATSVTSMSPONISLPASFPFS  
FHSPPHTAHNASVDMCELRKDLISLQFLOKOKASRRPSAPAOQOSLEKLS  
VAPMGMSFEEDRINATYWKLOPTAGLODILHRSOREQSEIMESYLPLEPTFOR  
TKRSGEAKRLVDFSSQALFODKNSCVLSEKVLGIVQNTKANTTEPVLTFO  
HQLQPNVTLCVFWEDPTLSFGHSSAGCEVRETQSCFNHLYFPAVAVSS  
VEVDVHKKHYLSLTVGCVSALACLVTIAVLCRVPVPCRRKRDYTIKVNALL  
LAVFLDTSFLISEPVALTGSSEGCASAIPLHFSLTCLSMGLGYLYLVVEVF  
GTYVPEYTLKLSMGWGPPIPLVTVALVDVNGPILIAVHRTPEGVLYPSMCVRD  
SLVSYTINIGLSIVPLFMAMATATVVOILRLRPRTORSHVLTLLGSLVIGLPM  
LIFPSFASGTFLVLYLPSITTSFQGLFIPTWYMRLOARGGPPLKSNDCALP  
ISSGSTSSRSI"

## ORIGIN

Query Match 95.5%; Score 21; DB 9; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGAGTTCTCGATGAGAT 21  
Db 348 TTTCGAGTTCTCGATGAGAT 328

RESULT 35  
AX029424/c 2834 bp DNA linear PAT 16-SEP-2000  
LOCUS  
DEFINITION Sequence 4 from Patent WO9915551.  
ACCESSION AX029424  
VERSION AX029424.1 GI:10190217  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Herzog, H.  
AUTHORS Novel receptor  
TITLE Patent: WO 9915551-A 4 01-APR-1999;  
JOURNAL GARVAN INST MED RES (AU) ; HERZOG HERBERT (AU)  
FEATURES location/Qualifiers  
1..2834  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 2834;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGAGTTCTCGATGAGAT 21  
Db 354 TTTCGAGTTCTCGATGAGAT 334

RESULT 36  
BD062446/c 2834 bp DNA linear PAT 27-AUG-2002  
LOCUS  
DEFINITION Novel receptor.  
ACCESSION BD062446  
VERSION BD062446.1 GI:22608049  
KEYWORDS JP 2001513653-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Herzog, H.  
AUTHORS Novel receptor  
TITLE Patent: JP 2001513653-A 2 04-SEP-2001;  
JOURNAL GARVAN INSTITUTE OF MEDICAL RESEARCH  
COMMENT OS Homo sapiens (human)  
PN JP 2001513653-A/2  
PD 04-SEP-2001  
PF 24-SEP-1998 JP 1999518348  
PR 24-SEP-1997 AU PO 9386  
PI HERBERT HERZOG  
PC C07K7/06, C07K14/705, C07K16/28, C12N15/12, C12N5/10, C12P21/02, PC  
A01K67/027, PC  
G01N33/68, C07H21/04

FF Key Location/Qualifiers.

FEATURES  
source 1..2834  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 95.5%; Score 21; DB 6; Length 2834;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGAGTTCTCGATGAGAT 21  
Db 354 TTTCGAGTTCTCGATGAGAT 334

RESULT 37  
AX965647/c 3564 bp DNA linear PAT 15-JAN-2004  
LOCUS  
DEFINITION Sequence 75 from Patent EP1375515.  
ACCESSION AX965647  
VERSION AX965647.1 GI:40974984  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Fukushima, D.M., Shibayama, S.M., and Tada, H.M.  
AUTHORS Polypeptide, cDNA encoding the same, and use thereof  
TITLE Patent: EP 1375515-A 75 02-JAN-2004;  
JOURNAL ONO PHARMACEUTICAL CO., LTD. (JP)  
FEATURES location/Qualifiers  
1..3564  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

source

1..3564  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## CDS

43..2106  
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 /protein\_id="CAF06561.1"  
 /db\_xref="GI:40974985"  
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 LLYGRDPLSDKASLLCFQHEESLAQPPPLATVTSWSPQNISLSPASFTFS  
 FHSPEPTAHNASVDMCELRDQLQLKHPQKASRSPSPASQOQLSESLTS  
 VRPMGDVNSFEEDRINATVWKLPQTPAGLDLHISROEEOSEIMESVILPRTLFOR  
 TKGREGEAKRLILVDFSSQALFODKNSOVGEKVLGIYVONTKVAHTEPVVLFQ  
 HOLOKRVTLQCVFVEDPTLSPGHSAGCEYRVRERQTSFCPNHLYEPVAVSS  
 VEADVANHGYLSLSYGVCSVALCLVSIAYILCSRRKPRPTTKVMHLLAVFL  
 DTFLLSEPVALTSEACRASAIPLHPSLTLCSMWGLSEGNLYRLVVEVGTYPG  
 YLLKLSAMGWGPIPLVTLVALVDVNDGPILLVHRTPEGVYPSMCIKRLSLVSI  
 TNLGFLSVLFENMAMLATMVQILRLRPHQKSHVTLGLSLVGLGIPALLIFSF  
 ASGRQLVVLVLFSLITSFGFLFIYWWSMLQARGGSPILKNSDSARLPISGSGT  
 SSSRI"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 3564;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCGATGAGAT 21  
 DB 228 TTCCGAGTTCGATGAGAT 208

RESULT 38  
 LOCUS AX061726 3686 bp DNA linear PAT 24-JUN-2001  
 DEFINITION Sequence 8 from Patent WO0100825.  
 ACCESSION AX061726  
 VERSION AX061726.1 GI:12539836

## SOURCE

ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 Dull, D. and Gorman, S.W.  
 Human chromosome 15 and 16 bardet-biedl syndrome polynucleotides,  
 polypeptides and methods of use  
 Patent: WO 0100825-A 8 04-JUN-2001;

## JOURNAL

CHIRON CORPORATION (US)

## FEATURES

source  
 1..3686  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 3686;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCGATGAGAT 21  
 DB 318 TTCCGAGTTCGATGAGAT 298

## RESULT 39

LOCUS BC008770 3702 bp mRNA linear PRI 29-JUN-2004

DEFINITION Homo sapiens G protein-coupled receptor 56, transcript variant 1,  
 mRNA (cDNA clone MGC:11409 IMAGE:3139174), complete cds.

ACCESSION BC008770  
 VERSION BC008770.2 GI:33869362

## KEYWORDS

MGC.  
 Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 3702)  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## AUTHORS

Strausberg, R., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diachenko, L., Marnett, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stadelton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mallaby, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Kuzny, D.M., Sodergren, E.U., Lu, X., Gibbs, R.A.,  
 Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butcherfield, Y.S., Krzywicki, M.I., Skalek, U., Small, D.E.,  
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

## TITLE

2 (bases 1 to 3702)  
 Strausberg, R.  
 Direct Submission  
 Submitted (25-MAY-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,  
 USA

## JOURNAL

NIH-MGC Project URL: <http://mgs.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:14250619.  
 Contact: MGC help desk  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc.mgsncbgrl.nih.gov

## REMARK

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 Series: IRL Plate: 4 Row: 9 Column: 2  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 19923767.  
 Location/Qualifiers  
 1..3702  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="MGC:1409 IMAGE:3139174"  
 /clone\_type="Placenta, choriocarcinoma"  
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 /lab\_host="DH10B-R"  
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VRFMDGMSFEEDRNATYKQPTFGDDIHHSQRESEINETSYLEPRITFOR
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Query Match 95.5%; Score 21; DB 9; Length 3702;  
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Qy 1 TTCGAGTTCGATGAGAT 21  
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 Db 344 TTCGAGTTCGATGAGAT 324

RESULT 40  
 CQ783397/c 3748 bp DNA linear PAT 17-MAR-2004  
 LOCUS CQ783397  
 DEFINITION Sequence 3537 from Patent EP1396543.  
 ACCESSION CQ783397  
 VERSION CQ783397.1 GI:45503325  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
 Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
 Koga, H.  
 Primers for synthesizing full length cDNA clones and their use  
 Patent: EP 1396543-A 3537 10-MAR-2004;  
 Research Association for Biotechnology (JP)

TITLE  
 JOURNAL  
 FEATURES  
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CDS

ORIGIN

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 LOCUS BD127626  
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BD127626  
 VERSION BD127626.1 GI:23222571  
 KEYWORDS JP 2002017375-A/3057.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,  
 Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and  
 Koga, H.  
 Primers for synthesizing full-length cDNA and use thereof  
 Patent: JP 2002017375-A 3057 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002017375-A/3057  
 PD 22-JAN-2002  
 PP 07-JUN-2000 JP 2000253172  
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO  
 PI ISHII,  
 PI YUKI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI  
 SHINICHI KOJIMA,  
 PI TETSUO OTSUKI, HISASHI KOGA  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
 10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
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 LOCUS AK075270  
 DEFINITION Homo sapiens cDNA FLJ90789 fls clone THYR01001523, highly similar  
 to Homo sapiens mRNA for TM7RN1 protein.  
 ACCESSION AK075270  
 VERSION AK075270.1 GI:22761246  
 KEYWORDS oligo capping; fls (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

**AUTHORS**  
 Isegai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masuno, Y., Ono, T., Okano, K., Yoshikawa, Y., Nishikawa, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Nimomiya, K.

**TITLE**  
 NEDO human cDNA sequencing project

**JOURNAL**  
 unpublished

**REFERENCE**  
 2 (bases 1 to 3748)  
 Isegai, T. and Otsuki, T.  
 Direct Submission

**AUTHORS**  
 Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

**JOURNAL**  
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert construction; Research Association for Biotechnology; cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.).

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 430 TTCCGAGTTCTCGATGAGAT 410

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 LOCUS AX136371  
 DEFINITION Sequence 293 from Patent EP1067182.  
 ACCESSION AX136371  
 VERSION AX136371.1 GI:14272777  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 1 Ota, T., Isegai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.  
 Secretory protein or membrane protein  
 Patent: EP 1067182-A 293 10-JAN-2001;  
 Helix Research Institute (JP)  
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**ORIGIN**  
 Query Match 95.5%; Score 21; DB 6; Length 3774;  
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 LOCUS BD123638  
 DEFINITION Secretory protein or membrane protein.  
 ACCESSION BD123638  
 VERSION BD123638.1 GI:23210583  
 KEYWORDS JP 2002017376-A/147.  
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 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 1 (bases 1 to 3774)  
 Ota, T., Isegai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.  
 Secretory protein or membrane protein  
 Patent: JP 2002017376-A 147 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 OS Homo sapiens (human)  
 PN JP 2002017376-A/147  
 PD 22-JAN-2002 JP 2002053173  
 PF 07-JUL-2000 JP 2000253173  
 PI TOSHIO OTA, TAKAO ISEGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU  
 PI SUGIYAMA,  
 PI KOJI HAYASHI  
 PC  
 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
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 DEFINITION Homo sapiens cDNA PSEC0255 file, clone NT2RP3003536, highly similar  
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 ACCESSION AK075555  
 VERSION AK075555.1 GI:22761780

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
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AUTHORS  
TITLE  
JOURNAL  
FEATURES  
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oligo capping; fls (full insert sequence).  
Homo sapiens (human)  
Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 Ota, T., Mashikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K., Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahara, K., Sugano, S. and Isogai, T.  
HRI human cDNA sequencing project  
Unpublished  
2 (bases 1 to 3774)  
Isogai, T. and Yamamoto, J.  
Direct Submission  
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
HRI human cDNA sequencing project; cDNA 5' - & 3' - end one pass sequencing; clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.  
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95.5%; Score 21; DB 9; Length 3774;  
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3819 bp DNA linear PAT 04-MAR-2004  
Sequence 482 from Patent EP1386931.  
CQ768015  
CQ768015.1 GI:45108767  
Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, J.  
Human neurotrophin homologue  
Patent: EP 1386931-A 482 04-FEB-2004;  
Genentech, Inc. (US)  
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AUTHORS  
TITLE  
JOURNAL  
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Db  
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Query Match  
Best Local Similarity  
Matches  
Db

AX358880/c  
AX358880  
Sequence 133 from Patent WO0193983.  
AX358880  
AX358880.1 GI:18675341  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding the same  
Patent: WO 0193983-A 133 13-DEC-2001;  
Genentech Inc. (US)  
Location/Qualifiers  
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95.5%; Score 21; DB 6; Length 3819;  
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3819 bp DNA linear PAT 15-FEB-2002  
Sequence 133 from Patent WO0208288.  
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AX362373.1 GI:18694644  
Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding the same  
Patent: WO 0208288-A 133 31-JAN-2002;  
Genentech, Inc. (US)  
Location/Qualifiers  
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 DEFINITION Sequence 91 from Patent WO0208284.  
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 VERSION AX454506.1 GI:21713877  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
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 REFERENCE  
 AUTHORS 1  
 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Maresters, S.A., Pan, J.,  
 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
 and Ye, W.  
 Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0208284-A 91 31-JAN-2002;  
 Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
 (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
 Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
 Hillan, Kenneth J. (US) ; Maresters, Scot A. (US) ; Pan, James (US)  
 ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
 Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
 I. (US)  
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 399 TTCCGAGTTCGATGAGAT 379  
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 AX464272/C  
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 DEFINITION Sequence 405 from Patent WO0140466.  
 ACCESSION AX464272  
 VERSION AX464272.1 GI:21899152  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS 1  
 Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,  
 Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,  
 Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
 Wood, W.I. and Zhang, Z.  
 Secreted and transmembrane polypeptides and nucleic acids encoding  
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 Patent: WO 0140466-A 405 07-JUN-2001;  
 Genentech Inc. (US)  
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 Best Local Similarity 100.0%; Pred.No. 41;  
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 399 TTCCGAGTTCGATGAGAT 379  
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Oy 1 TTCCGAGTTCGATGAGAT 21  
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Db 399 TTCCGAGTTCGATGAGAT 379  
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Search completed: February 2, 2005, 00:37:47  
 Job time : 1824 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 21:51:32 ; Search time 397 Seconds  
(without alignments)  
290.900 Million cell updates/sec

Title: US-10-073-054-14

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Sequence: 1 ttcgagcttcgcagtcgagatc 22

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

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- 2: Geneseq1990b:\*
- 3: Geneseq2000a:\*
- 4: Geneseq2001a:\*
- 5: Geneseq2002a:\*
- 6: Geneseq2003a:\*
- 7: Geneseq2004a:\*
- 8: Geneseq2005a:\*
- 9: Geneseq2006a:\*
- 10: Geneseq2007a:\*
- 11: Geneseq2008a:\*
- 12: Geneseq2009a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	21	95.5	22	ADA14227	ADA14227 GPR56 sen
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C 96	21	95.5	3819	9	ADB24764	AdB24764 Human PRO	C 169	21	95.5	3819	10	ADC63138	AdC63138 Human CDN
C 97	21	95.5	3819	9	ADA82288	AdA82288 Human PRO	C 170	21	95.5	3819	10	ADC68203	AdC68203 Human CDN
C 98	21	95.5	3819	9	ADA75251	AdA75251 Human PRO	C 171	21	95.5	3819	10	ADC41523	AdC41523 Human CDN
C 99	21	95.5	3819	9	ADA85329	AdA85329 Novel hum	C 172	21	95.5	3819	10	ADC67578	AdC67578 Human CDN
C 100	21	95.5	3819	9	ADA84777	AdA84777 Novel hum	C 173	21	95.5	3819	10	ADC62514	AdC62514 Human CDN
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C 102	21	95.5	3819	9	ADA80561	AdA80561 Human PRO	C 175	21	95.5	3819	10	ADC42147	AdC42147 Human CDN
C 103	21	95.5	3819	9	ADA75803	AdA75803 Human PRO	C 176	21	95.5	3819	10	ADC50446	AdC50446 Novel hum
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C 110	21	95.5	3819	9	ADA61065	AdA61065 Homo sapi	C 183	21	95.5	3819	10	ADC47460	AdC47460 Novel hum
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C 112	21	95.5	3819	9	ADA96541	AdA96541 Human PRO	C 185	21	95.5	3819	10	ADC57333	AdC57333 Novel hum
C 113	21	95.5	3819	9	ADA81113	AdA81113 Human PRO	C 186	21	95.5	3819	10	ADC60524	AdC60524 Novel hum
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C 115	21	95.5	3819	9	ADB26298	AdB26298 CDNA enco	C 188	21	95.5	3819	10	ADC55526	AdC55526 Human PRO
C 116	21	95.5	3819	9	ADB21783	AdB21783 Novel hum	C 189	21	95.5	3819	10	ADC54624	AdC54624 Novel hum
C 117	21	95.5	3819	9	ACD83242	ACD83242 Human sec	C 190	21	95.5	3819	10	ADC53585	AdC53585 Novel hum
C 118	21	95.5	3819	9	ACD29421	ACD29421 Novel hum	C 191	21	95.5	3819	10	ADC59108	AdC59108 Novel hum
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C 130	21	95.5	3819	9	ABT43948	ABT43948 Human mem	C 203	21	95.5	3819	10	ADC80590	AdC80590 Novel hum
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C 133	21	95.5	3819	9	ADB23660	AdB23660 Human PRO	C 206	21	95.5	3819	10	ADC77834	AdC77834 Novel hum
C 134	21	95.5	3819	9	ADA92382	AdA92382 Novel hum	C 207	21	95.5	3819	10	ADC80038	AdC80038 Novel hum
C 135	21	95.5	3819	9	ADB15445	AdB15445 Human PRO	C 208	21	95.5	3819	10	ADP11340	AdP11340 Human sec
C 136	21	95.5	3819	9	ADB83623	AdB83623 Novel hum	C 209	21	95.5	3819	10	ADP09507	AdP09507 Human PRO
C 137	21	95.5	3819	9	ADB80729	AdB80729 Novel hum	C 210	21	95.5	3819	10	ADP50797	AdP50797 Novel hum
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C 140	21	95.5	3819	9	ADB78352	AdB78352 Novel hum	C 213	21	95.5	3819	10	ADP51043	AdP51043 Novel hum
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C 142	21	95.5	3819	9	ADB66617	AdB66617 Novel hum	C 215	21	95.5	3819	10	ADP53651	AdP53651 Novel hum
C 143	21	95.5	3819	10	ADB85000	AdB85000 Human PRO	C 216	21	95.5	3819	10	ADP37133	AdP37133 Human PRO
C 144	21	95.5	3819	10	ADB89697	AdB89697 Human PRO	C 217	21	95.5	3819	10	ADP51807	AdP51807 CDNA enco
C 145	21	95.5	3819	10	ADB90429	AdB90429 Human PRO	C 218	21	95.5	3819	10	ADP02606	AdP02606 Human PRO
C 146	21	95.5	3819	10	ADB39530	AdB39530 Novel hum	C 219	21	95.5	3819	10	ADP50524	AdP50524 Human PRO
C 147	21	95.5	3819	10	ADB78106	AdB78106 Novel hum	C 220	21	95.5	3819	10	ADP02040	AdP02040 Human PRO
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C 151	21	95.5	3819	10	ADB47153	AdB47153 Novel hum	C 224	21	95.5	3819	10	ADP49516	AdP49516 Human CDN
C 152	21	95.5	3819	10	ADB83869	AdB83869 Novel hum	C 225	21	95.5	3819	10	ADP25539	AdP25539 Human PRO
C 153	21	95.5	3819	10	ADB86760	AdB86760 Human PRO	C 226	21	95.5	3819	10	ADP04435	AdP04435 Human PRO
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C 156	21	95.5	3819	10	ADB7365	AdB7365 Novel hum	C 229	21	95.5	3819	10	ADP22278	AdP22278 CDNA enco
C 157	21	95.5	3819	10	ADB34522	AdB34522 Human PRO	C 230	21	95.5	3819	10	ADP79502	AdP79502 Human CDN
C 158	21	95.5	3819	10	ADB35626	AdB35626 Human PRO	C 231	21	95.5	3819	10	ADP35570	AdP35570 Human CDN
C 159	21	95.5	3819	10	ADB33970	AdB33970 Human PRO	C 232	21	95.5	3819	10	ADP16684	AdP16684 Human CDN
C 160	21	95.5	3819	10	ADB35074	AdB35074 Human PRO	C 233	21	95.5	3819	10	ADP73299	AdP73299 Human CDN
C 161	21	95.5	3819	10	ADB36178	AdB36178 Novel hum	C 234	21	95.5	3819	10	ADP42038	AdP42038 Human PRO
C 162	21	95.5	3819	10	ADB46573	AdB46573 Novel hum	C 235	21	95.5	3819	10	ADP17855	AdP17855 Human PRO
C 163	21	95.5	3819	10	ADP44130	AdP44130 Human CDN	C 236	21	95.5	3819	10	ADP91987	AdP91987 Human PRO
C 164	21	95.5	3819	10	ADP61890	AdP61890 Human CDN	C 237	21	95.5	3819	10	ADP33450	AdP33450 Novel hum
C 165	21	95.5	3819	10	ADP63854	AdP63854 Human CDN	C 238	21	95.5	3819	10	ADP34002	AdP34002 Novel hum
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C 167	21	95.5	3819	10			C 240	21	95.5	3819	10		



C	387		21	95.5	3819	12	ADG58594	Adg58594 Novel hum	C	460	16.8	76.4	1238	10	ABo80357	Abq80357 A. fumigatus
C	388		21	95.5	3819	12	ADG70960	Novel hum	C	461	16.8	76.4	1504	3	AAc79921	Hac79921 Human sec
C	389		21	95.5	3819	12	ADH39039	Novel hum	C	462	16.8	76.4	6515	12	ADN06015	Adn06015 Antiposri-
C	390		21	95.5	3819	12	ADG58042	Novel hum	C	463	16.4	74.5	431	3	AAc46988	Aac46988 Arabidope
C	391		21	95.5	3819	12	ADG53626	Novel hum	C	464	16.4	74.5	441	11	ABD11644	Abd11644 Pseudomon
C	392		21	95.5	3819	12	ADG71512	Novel hum	C	465	16.4	74.5	703	10	ADK58302	Advk58302 Plant DNA
C	393		21	95.5	3819	12	ADG50655	Human CDN	C	466	16.4	74.5	1659	11	ABD11857	Abd11857 Pseudomoc
C	394		21	95.5	3819	12	ADG81659	Human PRO	C	467	16.4	74.5	3222	8	ACA42673	Aca42673 Prokaryot
C	395		21	95.5	3819	12	ADH30661	Human PRO	C	468	16.4	74.5	3267	11	ABD12103	Abd12103 Pseudomo
C	396		21	95.5	3819	12	ADH12028	Novel hum	C	469	16.4	74.5	3768	8	ABX11865	Abx11865 Stribits p
C	397		21	95.5	3819	12	ADG50003	Human CDN	C	470	16.2	73.6	168	6	ABN16138	Bbn16138 Human ORF
C	398		21	95.5	3819	12	ADG51903	Human CDN	C	471	16.2	73.6	461	9	ACH48110	Ach48110 Human lun
C	399		21	95.5	3819	12	ADG52450	Novel hum	C	472	16.2	73.6	467	6	ABV72644	Abv72644 Human his
C	400		21	95.5	3819	12	ADG554178	Novel hum	C	473	16.2	73.6	484	9	ACH30178	Ach30178 Human tes
C	401		21	95.5	3819	12	ADG49407	Human CDN	C	474	16.2	73.6	519	11	ABD15884	Abd15884 Pseudomor
C	402		21	95.5	3819	12	ADG81147	Human PRO	C	475	16.2	73.6	520	5	AAH87842	Aah87842 Peppermim
C	403		21	95.5	3819	12	ADG56386	Novel hum	C	476	16.2	73.6	534	8	ACA52981	Aca52981 Prokaryot
C	404		21	95.5	3819	12	ADH12652	Novel hum	C	477	16.2	73.6	568	6	ABQ42457	Abq42457 Oligonuc
C	405		21	95.5	3819	12	ADG48783	Human CDN	C	478	16.2	73.6	568	6	AAH87833	Aah87833 Oligonuc
C	406		21	95.5	3819	12	ADG61498	Novel hum	C	479	16.2	73.6	622	5	AAH87833	Aah87833 Oligonuc
C	407		21	95.5	3819	12	ADH28585	Human PRO	C	480	16.2	73.6	644	10	ADS66807	Ads66807 Plant DN
C	408		21	95.5	3819	12	ADG54730	Novel hum	C	481	16.2	73.6	649	3	AAF12142	Aaf12142 Aspergil11
C	409		21	95.5	3819	12	ADG59770	Novel hum	C	482	16.2	73.6	927	8	ABT21167	Abt21167 Aspergil11
C	410		21	95.5	3819	12	ADG51279	Human CDN	C	483	16.2	73.6	933	8	ABT19347	Abt19347 Aspergil11
C	411		21	95.5	3819	12	ADH43524	Human PRO	C	484	16.2	73.6	977	6	AEQ25056	Aeq25056 Oligonuc
C	412		21	95.5	3819	12	ADG59223	Human CDN	C	485	16.2	73.6	977	6	AEQ25057	Aeq25057 Oligonuc
C	413		21	95.5	3819	12	ADG34129	Novel hum	C	486	16.2	73.6	982	6	ABO24918	Abq24918 Oligonuc
C	414		21	95.5	3819	12	ADG62879	Human CDN	C	487	16.2	73.6	982	6	ABQ24919	Abq24919 O

PI Herzog H, Sutherland RL, Mackay CR, Henshall S;  
 XX WPI; 2003-689676/65.  
 DR  
 XX  
 PT New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.  
 XX  
 PS Claim 4; Page 125; 129pp; English.  
 CC The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumour growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytotactic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumour growth. The present sequence represents a GPR56 antisense  
 CC probe from the present invention.  
 CC  
 SQ Sequence 22 BP; 4 A; 4 C; 7 G; 7 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 22; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Gaps 0;  
 Matches 22; Conservative 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGATC 22  
 DB 1 TTGGAGTTCTCGATGAGATC 22  
 RESULT 2  
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 ID ADA14227 standard; DNA; 22 BP.  
 AC ADA14227;  
 XX 06-NOV-2003 (first entry)  
 DT  
 XX  
 DE GPR56 sense probe SEQ ID NO:11.  
 XX  
 KW human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;  
 KW GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;  
 KW gene therapy; probe; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003068965-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 12-FEB-2003; 2003WO-AU000178.  
 XX  
 PR 12-FEB-2002; 2002US-00073054.  
 XX  
 PA (GTWO-) G2 THERAPIES LTD.  
 XX  
 PI Herzog H, Sutherland RL, Mackay CR, Henshall S;  
 XX  
 DR WPI; 2003-689676/65.  
 XX  
 PT New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.  
 XX  
 PS Claim 2; Page 124; 129pp; English.

XX  
 CC The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumour growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytotactic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumour growth. The present sequence represents a GPR56 sense  
 CC probe from the present invention.  
 CC  
 SQ Sequence 22 BP; 7 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 4.1; Mismatches 0; Gaps 0;  
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 DB 22 TTGGAGTTCTCGATGAGAT 22  
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 ID AAX41171 standard; cDNA; 372 BP.  
 XX  
 AC AAX41171;  
 XX  
 DT 17-JUN-1999 (first entry)  
 XX  
 DE Human secreted protein 5' EST SEQ ID NO:115.  
 XX  
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;  
 KW forensic; gene therapy; chromosome mapping; signal peptide;  
 KW upstream regulatory sequence; cytokine activity; cell proliferation;  
 KW differentiation; haematopoiesis regulation; tissue growth regulation;  
 KW reproductive hormone regulation; chemokine; chemokine; haemostatic;  
 KW thrombolytic; anti-inflammatory; tumour inhibition; ds.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO9906548-A2.  
 XX  
 PD 11-FEB-1999.  
 XX  
 PF 31-JUL-1998; 98WO-IB001222.  
 XX  
 PR 01-AUG-1997; 97US-00905135.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Lacroix B;  
 XX  
 DR WPI; 1999-153778/13.  
 XX  
 DR P-PSDB; AAY12338.  
 XX  
 PT New nucleic acids encoding human secreted proteins - obtained from cDNA  
 PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,  
 PT umbilical cord, placenta and colon tissue.  
 XX  
 PS Claim 1; Page 274; 824pp; English.  
 CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for  
 CC human secreted proteins, and encode the proteins given in AAY12261 to  
 CC AAY12514, respectively. The proteins given represent the signal peptide  
 CC and an N-terminal fragment of a secreted protein. The nucleic acid  
 CC sequences can be used for producing secreted human gene products. They

CC can also be used to develop products for diagnosis and therapy. The  
 CC proteins obtained may have cytokine activity, haematopoietic regulating  
 CC proliferation/differentiation activity, haematopoietic hormone  
 CC activity, tissue growth regulating activity, reproductive hormone  
 CC regulating activity, chemokine/chemokine activity, haemostatic and  
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, tumour inhibition activity or other activities. The products  
 CC can be used in forensic, gene therapy and chromosome mapping procedures.  
 CC The sequences can also be used for obtaining corresponding promoter  
 CC sequences. The nucleic acids encoding the signal peptide can be used for  
 CC directing extracellular secretion of a polypeptide or the insertion of a  
 CC polypeptide into a membrane, or importing a polypeptide into a cell  
 CC

SO Sequence 372 BP; 92 A; 115 C; 104 G; 55 T; 0 U; 6 Other;

Query Match 95.5%; Score 21; DB 2; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21  
 Db 369 TTCGAGTTCTCGATGAGAT 349

RESULT 4  
 AA127155/c  
 ID AA127155 standard; DNA; 423 BP.  
 AC AA127155;  
 XX  
 XX 12-OCT-2001 (first entry)  
 DT  
 DE Probe #17088 for gene expression analysis in human cervical cell sample.  
 KW Probe: human; microarray; gene expression; cervical epithelial cell;  
 KW cervical cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157278-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000670.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488901/53.  
 DR  
 XX human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human cervical epithelial cells.  
 XX  
 XX Claim 25; SEQ ID NO 17088; 487bp; English.

CC The present invention relates to human single exon nucleic acid probes  
 CC (SNP). The present sequence is one such probe. The SNPs are derived  
 CC from human HeLa cells. The SNPs can be used to produce a single exon  
 CC microarray, which can be used for measuring human gene expression in a  
 CC sample derived from human cervical epithelial cells. By measuring gene  
 CC expression, the probes are therefore useful in grading and/or staging of  
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SO Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 4; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21  
 Db 122 TTCGAGTTCTCGATGAGAT 102

RESULT 5  
 ABA75435/c  
 ID ABA75435 standard; DNA; 423 BP.  
 AC ABA75435;  
 XX  
 XX 01-FEB-2002 (first entry)  
 DT  
 DE Human foetal liver single exon nucleic acid probe #23740.  
 DE Human foetal liver single exon nucleic acid probe #23740.  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157277-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483447/52.  
 DR  
 XX human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human foetal liver.  
 XX  
 XX Claim 4; SEQ ID NO 23740; 639bp + Sequence Listing; English.

CC The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human foetal liver. The  
 CC present sequence is a single exon nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 CC

SO Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 4; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATGAGAT 21  
 Db 122 TTCGAGTTCTCGATGAGAT 102

RESULT 6



AA156007/c  
ID AA156007 standard; DNA; 423 BP.  
XX  
AC AA156007;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Probe #24693 used to measure gene expression in human placenta sample.  
XX  
KM Probe; microarray; human; placenta; antenatal diagnosis;  
KM genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
PS Claim 25; SEQ ID NO 24693; 654bp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SENP).  
CC The present sequence is one such probe. The probes are useful for  
CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders  
XX  
SQ Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
XX  
Query Match 95.5%; Score 21; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 TTGGAGTTCGATGAGAT 21  
DB 122 TTGGAGTTCGATGAGAT 102  
XX  
RESULT 7  
ABA40063/c  
ID ABA40063 standard; DNA; 423 BP.  
XX  
AC ABA40063;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
PF Probe #18529 for gene expression analysis in human heart cell sample.  
XX  
DE Human; gene expression; heart; microarray; vascular system; probe;  
XX cardiovascular disease; hypertension; cardiac arrhythmia;  
KM congenital heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157274-A2.

XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000666.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts.  
XX  
PS Claim 4; SEQ ID NO 18529; 530bp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,  
CC monitoring and prognosing diseases of the human heart and vascular system  
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
CC congenital heart disease. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences  
XX  
SQ Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
XX  
Query Match 95.5%; Score 21; DB 4; Length 423;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 TTGGAGTTCGATGAGAT 21  
DB 122 TTGGAGTTCGATGAGAT 102  
XX  
RESULT 8  
AAK50067/c  
ID AAK50067 standard; DNA; 423 BP.  
XX  
AC AAK50067;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed single exon probe SEQ ID NO: 24624.  
XX  
KM Human; bone marrow expressed exon; gene expression analysis; probe;  
KM microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000668.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.

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PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488900/53.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 24624; 658bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
XX Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;
SQ
Query Match 95.5%; Score 21; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGAGTTCTCGATGGAGAT 21
Db 122 TTCCGAGTTCTCGATGGAGAT 102
XX
XX RESULT 9
XX ID AAK24002 standard; DNA; 423 BP.
XX AAK24002;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 23993.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX SB.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-483446/52.
XX DR
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brain.
XX
XX Example 4; SEQ ID NO 23993; 650bp + Sequence Listing; English.
XX

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CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
XX Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;
SQ
Query Match 95.5%; Score 21; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGAGTTCTCGATGGAGAT 21
Db 122 TTCCGAGTTCTCGATGGAGAT 102
XX
XX RESULT 10
XX ID ABS49706 standard; DNA; 423 BP.
XX ABS49706;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver single exon probe, SEQ ID NO 24696.
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
XX hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
XX coronary heart disease; SB.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488898/53.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
XX Claim 4; SEQ ID NO 24696; 658bp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENp) (1) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 1109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (1) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

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CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
 SQ Query Match 95.5%; Score 21; DB 4; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCGATGAGAT 21  
 DB 122 TTGGAGTTCGATGAGAT 102  
 RESULT 11  
 ABS23554/C  
 ID ABS23554 standard; DNA; 423 BP.  
 AC ABS23554;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 23545.  
 XX  
 KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease; open reading frame; ORF.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-0063236P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 measure gene expression in human lung samples.  
 XX  
 PS Claim 4; SEQ ID NO 23545; 634bp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 nucleic acid probes for measuring gene expression in a sample derived  
 from human lung comprising single exon nucleic acid probes having one of  
 12614 nucleic acid sequences mentioned in the specification, or their  
 complements or the 12387 open reading frames derived from the 12614  
 probes. Also included are a microarray comprising the novel set of probes  
 ; the novel set of probes which hybridise at high stringency to a nucleic  
 acid expressed in the human lung; measuring gene expression in a sample  
 derived from human lung, comprising (a) contacting the array with a  
 collection of detectably labeled nucleic acids derived from human lung  
 mRNA, and (b) measuring the label detectably bound to each probe of the  
 array; identifying exons in a eukaryotic genome, comprising (a)  
 algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray, assigning exons to a single gene.  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe open reading frame of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 423 BP; 85 A; 163 C; 92 G; 83 T; 0 U; 0 Other;  
 XX  
 QY Query Match 95.5%; Score 21; DB 6; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 122 TTGGAGTTCGATGAGAT 102  
 QY 1 TTGGAGTTCGATGAGAT 21  
 DB 122 TTGGAGTTCGATGAGAT 102  
 RESULT 12  
 ADL40560/C  
 ID ADL40560 standard; DNA; 493 BP.  
 XX  
 AC ADL40560;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human ovarian cancer DNA marker #14450.  
 XX  
 KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200170979-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 21-MAR-2001; 2001WO-US009126.  
 XX  
 PR 21-MAR-2000; 2000US-0191031P.  
 PR 25-MAY-2000; 2000US-0207124P.  
 PR 15-JUN-2000; 2000US-0211940P.  
 PR 07-JUL-2000; 2000US-0216820P.  
 PR 25-JUL-2000; 2000US-0220661P.  
 PR 21-DEC-2000; 2000US-0257672P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Lee J, Lillie J;  
 XX  
 DR WPI; 2001-611502/70.  
 XX  
 PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian  
 cancer cells as compared to their normal non-cancerous ovarian cells are  
 used to characterize stage, grade, histological type of ovarian cancer.

XX PS Disclosure; SEQ ID NO 14450; 106bp; English.  
CC The invention relates to nucleic acid markers which are overexpressed in  
CC ovarian cancer cells as compared to their expression in normal (i.e. non-  
CC cancerous) ovarian cells. The invention also relates to polypeptides  
CC encoded by the markers, antibodies that selectively bind to the  
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk  
CC of developing ovarian cancer involving inhibiting expression of a gene  
CC corresponding to a marker of the invention and a method of treating a  
CC patient afflicted with ovarian cancer comprising providing to cells of  
CC the patient an antisense oligonucleotide complementary to a marker of the  
CC invention. The markers are useful for assessing if a patient is afflicted  
CC with ovarian cancer, which involves comparing the level of expression of  
CC a marker in a patient sample and a normal level of expression of the  
CC marker in a control non-ovarian cancer sample. A difference between the  
CC expression levels indicates ovarian cancer. The level of expression of a  
CC marker corresponds to a secreted protein or to a transcribed  
CC polynucleotide or its portion. The level of expression of the marker is  
CC assessed by detecting the presence in the sample, a protein or protein  
CC fragment corresponding to the marker. The presence of protein or protein  
CC fragment is detected using an antibody that specifically binds with the  
CC protein or protein fragment. Alternatively, the level of expression of  
CC the marker is assessed by detecting the presence of a transcribed  
CC polynucleotide which anneals with the marker or anneals with a portion of  
CC the polynucleotide comprising the marker, under stringent conditions. The  
CC marker is also used for monitoring the progression of ovarian cancer in a  
CC patient which involves detecting expression of the marker in a patient  
CC sample at a first point in time, repeating the method at a subsequent  
CC time and comparing the level of expression. The method is carried out  
CC using an ovarian tissue sample. A composition comprising a marker,  
CC polypeptide or antibody of the invention is used to treat ovarian cancer.  
CC This sequence represents a human ovarian cancer DNA marker of the  
CC invention.  
XX  
SQ Sequence 493 BP; 93 A; 171 C; 130 G; 99 T; 0 U; 0 Other;  
Query Match 95.5%; Score 21; DB 5; Length 493;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGTTCTCGATGGAGAT 21  
Db 416 TTGGAGTTCTCGATGGAGAT 396  
RESULT 13  
ADQ20571/c  
ID ADQ20571 standard; DNA; 527 BP.  
XX  
AC ADQ20571;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3391.  
XX  
KW soft tissue sarcoma; cytotactic; gene therapy; vaccine; screening; human;  
XX ds.  
XX Homo sapiens.  
XX PN WO2004048938-A2.  
XX PD 10-JUN-2004.  
XX PF 26-NOV-2003; 2003WO-US038193.  
XX PR 26-NOV-2002; 2002US-0429739P.  
XX PA (PROT-) PROTEIN DESIGN LABS INC.  
XX PI Aziz N, Ginsburg WM, Zlotnick A;  
XX

DR WPI; 2004-441208/41.  
XX  
PT Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.  
XX  
PS Example 2; SEQ ID NO 3391; 210bp; English.  
XX  
CC The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in the first soft tissue sample, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method for detecting soft tissue  
CC cytotactic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC DNA of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.  
XX  
SQ Sequence 527 BP; 106 A; 186 C; 128 G; 107 T; 0 U; 0 Other;  
Query Match 95.5%; Score 21; DB 12; Length 527;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGTTCTCGATGGAGAT 21  
Db 247 TTGGAGTTCTCGATGGAGAT 227  
RESULT 14  
AA118016/c  
ID AA118016 standard; DNA; 582 BP.  
XX  
AC AA118016;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Probe #7949 for gene expression analysis in human cervical cell sample.  
XX  
KW Probe; human; microarray; gene expression; cervical epithelial cell;  
XX cervical cancer; ss.  
XX  
OS Homo sapiens.  
XX PN WO200157278-A2.  
XX PD 09-AUG-2001.  
XX PF 30-JAN-2001; 2001WO-US000670.  
XX PR 04-FEB-2000; 2000US-0180312P.  
XX PR 26-MAY-2000; 2000US-0207456P.  
XX PR 30-JUN-2000; 2000US-00608408.  
XX PR 03-AUG-2000; 2000US-00632366.  
XX PR 21-SEP-2000; 2000US-0234687P.  
XX PR 27-SEP-2000; 2000US-0236359P.  
XX PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488901/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human cervical epithelial cells.  
XX  
PS Claim 25; SEQ ID NO 7949; 487bp; English.

XX The present invention relates to human single exon nucleic acid probes  
CC (SNP). The present sequence is one such probe. The SNPs are derived  
CC from human HeLa cells. The SNPs can be used to produce a single exon  
CC microarray, which can be used for measuring human gene expression in a  
CC sample derived from human cervical epithelial cells. By measuring gene  
CC expression, the probes are therefore useful in grading and/or staging of  
CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 4; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 5.2;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21

DB 227 TTCGAGTTCGATGAGAT 207

RESULT 15

ABA62983/C

ID ABA62983 standard; DNA; 582 BP.

AC ABA62983;

DT 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #11288.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

XX WO200157272-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000669.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human foetal liver.

XX Claim 1; SEQ ID NO 11288; 639bp + Sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human foetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX Query Match 95.5%; Score 21; DB 4; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 5.2;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21

DB 227 TTCGAGTTCGATGAGAT 207

RESULT 16

AA143010/C

ID AA143010 standard; DNA; 582 BP.

AC AA143010;

DT 17-OCT-2001 (first entry)

XX Probe #11696 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder; ss.

OS Homo sapiens.

XX WO200157272-A2.

PN 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US000663.

PF 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 25; SEQ ID NO 11696; 654bp; English.

XX The present invention relates to single exon nucleic acid probes (SNP).

XX The present sequence is one such probe. The probes are useful for

XX producing a microarray for predicting, measuring and displaying gene

XX expression in samples derived from human placenta. The probes are useful

XX for antenatal diagnosis of human genetic disorders

XX Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 4; Length 582;

XX Best Local Similarity 100.0%; Pred. No. 5.2;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21

DB 227 TTCGAGTTCGATGAGAT 207

RESULT 17

ABA30246/C

ID ABA30246 standard; DNA; 582 BP.

AC ABA30246;

DT 23-JAN-2002 (first entry)

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XX DE Probe #8712 for gene expression analysis in human heart cell sample.
XX XX
XX KM Human; gene expression; heart; microarray; vascular system; probe;
XX KM cardiovascular disease; hypertension; cardiac arrhythmia;
XX KM congenital heart disease; ss.
XX OS Homo sapiens.
XX XX MO200157274-A2.
XX PN 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA
XX PI (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-48899/53.
XX XX
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 1; SEQ ID NO 8712; 530bp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease. Note: The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX CC
XX SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;
XX
XX Query Match 95.5%; Score 21; DB 4; Length 582;
XX Best Local Similarity 100.0%; Pred. No. 5.2;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGGAGTTCTCGATGAGAT 21
XX Db 227 TTGGAGTTCTCGATGAGAT 207
XX
XX RESULT 18
XX ID AAK37182/c
XX ID AAK37182 standard; DNA; 582 BP.
XX XX
XX AC AAK37182;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 11739.
XX XX
XX KM Human; bone marrow expressed exon; gene expression analysis; probe;
XX KM microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN MO200157276-A2.

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XX XX
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA
XX PI (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-48899/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX XX
XX PS Example 4; SEQ ID NO 11739; 658bp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX CC the probes of the invention
XX CC
XX SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;
XX
XX Query Match 95.5%; Score 21; DB 4; Length 582;
XX Best Local Similarity 100.0%; Pred. No. 5.2;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGGAGTTCTCGATGAGAT 21
XX Db 227 TTGGAGTTCTCGATGAGAT 207
XX
XX RESULT 19
XX ID AAK11396/c
XX ID AAK11396 standard; DNA; 582 BP.
XX XX
XX AC AAK11396;
XX XX
XX DT 05-NOV-2001 (first entry)
XX XX
XX DE Human brain expressed single exon probe SEQ ID NO: 11387.
XX XX
XX KM Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX KM ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN MO200157275-A2.
XX PD
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA
XX PI (MOLE-) MOLECULAR DYNAMICS INC.

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XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI, 2001-483446/52.  
 DR Single exon nucleic acid probes for analyzing gene expression in human  
 XX brains.  
 PT Example 4; SEQ ID NO 11387; 650bp + Sequence Listing; English.  
 XX  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention  
 CC  
 SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 4; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TTCGAGTTCGATGAGAT 21  
 DB 227 TTCGAGTTCGATGAGAT 207  
 RESULT 20  
 ABS36856/C  
 ID ABS36856 standard; DNA; 582 BP.  
 XX  
 AC ABS36856;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Human liver single exon probe, SEQ ID NO 11846.  
 XX  
 DE Human single exon nucleic acid probe; liver; cirrhosis;  
 KW hyperlipoproteinemia; hyperlipidaemia; hypercholesterolaemia;  
 KW coronary heart disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000664.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI, 2001-488898/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human adult liver.  
 XX  
 PS Claim 1; SEQ ID NO 11846; 656bp; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridizes at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (I) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
 CC liver single exon nucleic acid probes of the invention. Note: The  
 CC sequence information for this patent does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 4; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TTCGAGTTCGATGAGAT 21  
 DB 227 TTCGAGTTCGATGAGAT 207  
 RESULT 21  
 ABS11174/C  
 ID ABS11174 standard; DNA; 582 BP.  
 XX  
 AC ABS11174;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human genome-derived single exon probe from lung SEQ ID NO 11165.  
 XX  
 DE Human; de; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hereditary-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI, 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX  
 PS Claim 1; SEQ ID NO 11165; 634bp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridize at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC collected from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Rudaik syndrome, sarcoidosis, pulmonary haemorrhoidosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 582 BP; 114 A; 216 C; 136 G; 116 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 6; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 5.2;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCGAGTTCTCGATGAGAT 21  
 |||||  
 DB 227 TTTCGAGTTCTCGATGAGAT 207

RESULT 22  
 ID AAK92315/C  
 ID AAK92315 standard; cDNA; 739 BP.

AC AAK92315;  
 DT 06-NOV-2001 (first entry)  
 DE Human cDNA 5'-end sequence, SEQ ID NO: 775.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUN-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 DR WPI; 2001-524255/58.  
 PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.

PS Claim 2; SEQ ID NO 775; 1380bp + Sequence Listing; English.

CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is the nucleotide sequence of the 5'-end of  
 CC a cDNA provided in the invention. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in CD-  
 CC ROM format directly from EPO

SQ Sequence 739 BP; 146 A; 242 C; 192 G; 155 T; 0 U; 4 Other;  
 Query Match 95.5%; Score 21; DB 4; Length 739;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCGAGTTCTCGATGAGAT 21  
 |||||  
 DB 430 TTTCGAGTTCTCGATGAGAT 410

RESULT 23  
 ID AAK93857/C  
 ID AAK93857 standard; cDNA; 739 BP.

AC AAK93857;  
 DT 06-NOV-2001 (first entry)

DE Human cDNA clone representative sequence, SEQ ID NO: 2317.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUN-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 DR WPI; 2001-524255/58.

PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.

PS Example 11; SEQ ID NO 2317; 1380bp + Sequence Listing; English.

CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesized by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence was used as the representative sequence  
 CC from a human clone which was used in homology searches to identify the  
 CC clone. Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in CD-ROM format directly from  
 CC EPO

SQ Sequence 739 BP; 146 A; 242 C; 192 G; 155 T; 0 U; 4 Other;

Query Match 95.5%; Score 21; DB 4; Length 739;

Best Local Similarity 100.0%; Pred. No. 5.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
 |||||  
 DB 430 TTGGAGTTCGATGAGAT 410

RESULT 24

ADL28742/C  
 ID ADL28742 standard; cDNA; 739 BP.

XX ADL28742;

DT 20-MAY-2004 (first entry)

XX 5' end of a human cDNA molecule Segid 775.

XX human; medicine; signal transduction; glycoprotein; transcription;

KW oligo-capping method; ss.

XX Homo sapiens.

XX EPI396543-A2.

PD 10-MAR-2004.

XX 07-JUL-2000; 2003EP-00025638.

XX 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-0018774.

PR 02-MAY-2000; 2000JP-00183865.

PR 07-JUL-2000; 2000EP-00114089.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2004-204755/20.

XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full

PT length human cDNAs.

XX Disclosure; SEQ ID NO 775; 1340bp; English.

XX This invention relates to a novel primers useful for synthesizing full

CC length cDNA molecules that encode human proteins. Specifically, it refers

CC to secretory or membrane proteins that are potential therapeutic agents/

CC target molecules in the field of medicine, and in particular genes

CC encoding proteins that are associated with signal transduction, a method

CC for efficiently cloning a full length human cDNA from both the 5' and 3'

CC ends using the oligo-capping method. This polynucleotide sequence is the

Best Local Similarity 100.0%; Pred. No. 5.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
 |||||  
 DB 430 TTGGAGTTCGATGAGAT 410

RESULT 25

ADL30284/C  
 ID ADL30284 standard; cDNA; 739 BP.

XX ADL30284;

DT 20-MAY-2004 (first entry)

XX 3' end of a representative human cDNA cluster Segid 2317.

XX human; medicine; signal transduction; glycoprotein; transcription;

KW oligo-capping method; ss.

XX Homo sapiens.

XX EPI396543-A2.

PD 10-MAR-2004.

XX 07-JUL-2000; 2003EP-00025638.

XX 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-0018774.

PR 02-MAY-2000; 2000JP-00183865.

PR 07-JUL-2000; 2000EP-00114089.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2004-204755/20.

XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full

PT length human cDNAs.

XX Example 18; SEQ ID NO 2317; 1340bp; English.

XX This invention relates to a novel primers useful for synthesizing full

CC length cDNA molecules that encode human proteins. Specifically, it refers

CC to secretory or membrane proteins that are potential therapeutic agents/

CC target molecules in the field of medicine, and in particular genes

CC encoding proteins that are associated with signal transduction, a method

CC for efficiently cloning a full length human cDNA from both the 5' and 3'

CC ends using the oligo-capping method. This polynucleotide sequence is the

CC 3' end of a representative human DNA cluster of the invention.

SQ Sequence 739 BP; 146 A; 242 C; 192 G; 155 T; 0 U; 4 Other;

Query Match 95.5%; Score 21; DB 12; Length 739;

Best Local Similarity 100.0%; Pred. No. 5.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
 |||||  
 DB 430 TTGGAGTTCGATGAGAT 410

RESULT 26

AAF94095/C  
 ID AAF94095 standard; DNA; 745 BP.

XX AAF94095;



PI Chawla NK, Yue H, Richardson TW, Marcuis JP, Lehr-Mason PM;  
PI Govard AE, Becha SP, Kable AE, Swarnakar A, Jin P, Hawkins PR;  
PI Chien D, Rammumar J, Tran UK, Hafalia AA, Baughn MR, Lee SY;  
PI Jiang X, Jackson AA, Khare R, Bulloch SA;  
XX WPJ: 2003-697610/66.  
DR P-PSDB: ADA09870.  
XX  
XX  
PT New human receptor and membrane associated proteins and nucleic acids,  
PT useful for diagnosing, treating or preventing e.g. viral, bacterial,  
PT fungal, parasitic, protozoan or helminthic infections, cancers,  
PT neurological disorders.  
XX  
XX  
XX Claim 5; Page 276; 298pp; English.  
XX  
XX The invention relates to 38 human receptors and membrane-associated  
CC proteins (REMAP), REMAP-1 to REMAP-38, and the cDNAs encoding them  
CC (ADA09859-ADA09934). The invention also encompasses expression  
CC constructs, host cells and transgenic organisms comprising a REMAP  
CC nucleic acid sequence; the recombinant preparation of a REMAP; an  
CC antibody against a REMAP; methods of detection of REMAP proteins or  
CC nucleic acids; a micro-array containing REMAP nucleic acids; methods of  
CC screening compounds for their ability to modulate REMAP activity or  
CC expression; and pharmaceutical compositions comprising a REMAP protein, a  
CC REMAP agonist or REMAP antagonist. The REMAP proteins, nucleic acids or  
CC compositions comprising them are useful in diagnosing, treating or  
CC preventing a variety of disorders, including cell proliferative disorders  
CC (e.g., arteriosclerosis, cirrhosis, hepatitis, psoriasis, or primary  
CC thrombocytopenia) or cancers (e.g., adenocarcinoma, leukemia, or cancers  
CC of the bone, brain, breast or uterus); autoimmune/inflammatory disorders  
CC (e.g., AIDS, allergies, anaemia, asthma, bronchitis, gout, multiple  
CC sclerosis, osteoarthritis, rheumatoid arthritis, or systemic lupus  
CC erythematosus); viral, bacterial, fungal, parasitic, protozoan or  
CC helminthic infections; neurological disorders (e.g., epilepsy, stroke,  
CC Alzheimer's disease, dementia, or Parkinson's disease); metabolic  
CC disorders (e.g., hereditary fructose intolerance, obesity, hypoglycaemia  
CC or diabetes); developmental disorders (e.g., achondroplastic dwarfism,  
CC hypothyroidism or hydrocephalus); or endocrine disorders (e.g., disorders  
CC of the hypothalamus or pituitary gland). The present sequence represents  
CC a REMAP cDNA of the invention. Note: Additional single nucleotide  
CC polymorphisms (SNPs) are given for this sequence at positions 193, 572,  
CC 625 and 693; however, for each of these, neither variant disclosed  
CC matches the nucleotide given in the sequence.  
XX  
SQ Sequence 1142 BP; 269 A; 343 C; 281 G; 249 T; 0 U; 0 Other;  
Query Match 95.5%; Score 21; DB 9; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
DY 1 TTCGAGTTCGATGAGAT 21  
|||  
Db 281 TTCGAGTTCGATGAGAT 261  
|||  
RESULT 28  
AAK35742/c  
ID AAK35742 standard; cDNA, 2061 BP.  
XX  
XX AAK35742;  
XX  
XX  
DT 09-JUL-1999 (first entry)  
XX  
XX cDNA encoding a protein identified by the signal sequence trap method.  
XX  
XX Signal sequence trap method; SRT method; immunisation; inhibition;  
XX infection; allergy; cancer; regulation; tissue formation; tissue repair;  
XX activin activity; inhibin activity; chemokine activity;  
XX cytokine activity; blood coagulation regulation; agonist; antagonist;  
XX metabolic disorder; hormonal disorder; immune disorder;  
XX severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;  
XX  
XX  
XX

	Homo sapiens.
PX	MOS918126-AI.
XX	15-APR-1999.
FJ	06-OCT-1998;
PF	98WO-JP004514.
PP	07-OCT-1997;   97JP-00274674.
PR	(ONOX ) ONO PHARM CO LTD.
PA	Fukushima D, Shibayama S, Tada H;
P1	WPI; 1999-277254/23.
DR	P-PADB; AAY02382.
XX	Polypeptides identified by the signal sequence trap method from a human PT cDNA library..
PS	Claim 4; Page 231-232; 281pp; Japanese.
CC	AAY35694-135747 represent cDNA sequences that encode novel polypeptides CC (AAY02358-84) which are identified from a human placental cDNA library by the signal sequence trap (SST) method. The polypeptides have a broad range of physiological activity, including immunisation against and inhibition of infections, allergies and cancer; regulation of tissue formation and repair; activin/inhibin activity; chemokine/cytokine activity; blood coagulation regulation; and receptor/ligand agonist or antagonist activity. The polypeptides can be used for prevention and treatment of disorders including infections by bacteria, yeasts and viruses (including HIV) and protozoa; metabolic and hormonal disorders; immune disorders (including severe combined immunodeficiency (SCID) and AIDS; thrombosis; cancer; and traumatic or surgical wounds
SQ	Sequence 2061 BP; 384 A; 699 C; 541 G; 437 T; 0 U; 0 Other;
OY	Query Match                 95.5%; Score 21; DB 2; Length 2061; Best Local Similarity      100.0%; Prod. No. 5.7; Mismatches   0; Indels   0; Gaps   0. Matches   21; Conservative   0; Mismatches
Df	1 TTTCGAGTTCTCGATGGAGAT 21              Db          186 TTCGAGTTCGCATGGAGAT 166
RESULT 29	
ID	ADO29927/C
AC	ADO29927 standard; CDNA; 2064 BP.
XX	ADO29927;
DT	29-Jul-2004 (first entry)
DE	Human GPCR GPRS6 polynucleotide, SEQ ID NO:1029.
KM	G protein-coupled receptor; GPCR; drug screening; diagnosis;
KM	transgenic mouse; neurological disorder; adrenal gland disorder;
KM	colon disorder; intestinal disorder; cardiovascular disorder;
KM	muscular disorder; blood disorder; immune disorder; bone disorder;
KM	joint disorder; metabolic disorder; nutritive disorder; cancer;
KM	kidney disorder; liver disorder; lung disorder; breast disorder;
KM	ovary disorder; uterus disorder; prostate disorder; testis disorder;
KM	skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KM	thyms disorder; thyroid disorder; antiparkinsonian; anti-nauseic;
KM	Cystostatic; anti-inflammatory; vasodilator; antianginal; antiarrhythmic;
KM	CNS; central nervous system; respiratory; antididiabetic; antidiabetic;
KM	viralicide; hepatotropic; antibacterial; antianaemic; antisobornetic;
KM	immunological; anticancer; antithyroid; antiallergic; anorectic;
KM	immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
gene; se.	
XX	
OS	Homo sapiens.

XX MO2004040000-A2.  
 XX 13-MAY-2004.  
 XX 09-SEP-2003; 2003WO-US028226.  
 XX 09-SEP-2002; 2002US-0409303P.  
 XX 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRIMAL INC.  
 XX Galenaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,  
 XX Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX WPI; 2004-390329/36.  
 XX P-PSDB; ADO29416.  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 XX compounds that modulates diagnosing and treating disease condition  
 XX associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 XX pectoris, Parkinson's disease.  
 XX Claim 151; SEQ ID NO 1029; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors  
 XX (GPCRs) and nucleic acids encoding them. The invention also relates to  
 XX sequences at least 90% identical to the GPCR proteins and nucleic acids  
 XX of the invention; methods of treating, preventing or diagnosing diseases  
 XX associated with GPCRs of the invention; methods of screening for  
 XX compounds useful in the treatment of GPCR-related diseases; a transgenic  
 XX mouse comprising a GPCR gene of the invention; a mouse comprising a  
 XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 XX from the transgenic mice; kits comprising several mice, each of which has  
 XX a mutation in a different GPCR gene of the invention; and kits comprising  
 XX probes which hybridize to GPCR polynucleotides of the invention. The  
 XX invention further discloses variants of the GPCR polypeptides and vectors  
 XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 XX be used in the diagnosis, treatment or prevention of a wide variety of  
 XX diseases including neurological disorders (e.g., Alzheimer's disease,  
 XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 XX disorders of the adrenal gland; disorders of the colon or intestine  
 XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 XX myocardial infarction); muscular disorders; blood disorders (e.g.,  
 XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 XX diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 XX thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 XX nucleic acid of the invention. Note: The full sequence data for this  
 XX patent did not form part of the printed specification; those sequences  
 XX not shown were obtained in electronic format directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pcr\_sequences.

XX Sequence 2064 BP; 384 A; 701 C; 541 G; 438 T; 0 U; 0 Other;  
 XX  
 XX Query Match 95.5%; Score 21; DB 12; Length 2064;  
 XX Best Local Similarity 100.0%; Pred. No. 5.7;  
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTCGAGTTCTCGATGAGAT 21  
 XX |||||  
 XX DB 186 TTTCGAGTTCTCGATGAGAT 166  
 XX  
 XX RESULT 30  
 XX AAD39154/C  
 XX ID AAD39154 standard; cDNA; 2082 BP.  
 XX AC AAD39154;

XX 04-OCT-2002 (first entry)  
 XX Human AP4AR cDNA.  
 XX Human; diadenosine tetraphosphate receptor; G-protein coupled receptor;  
 XX cardiovascular disorder; central nervous system disorder; hypertension;  
 XX cardioprotective activity; genitourinary system disorder; vasodilation;  
 XX myocardial ischaemia; immunological disorder; prophylaxis; AP4AR; AP4A;  
 XX GPR56; vaccine; therapy; gene; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 1..2082  
 XX FT /\*tag= a  
 XX FT /product= "Human AP4AR protein"

XX WO200234781-A1.  
 XX 02-MAY-2002.  
 XX 16-OCT-2001; 2001WO-EP011953.  
 XX 20-OCT-2000; 2000EP-00122836.  
 XX (SOLV ) SOLVAY PHARM GMBH.  
 XX Berger C, Tulp MM, Van RJ;  
 XX WPI; 2002-479707/51.  
 XX P-PSDB; AAE24077.  
 XX Identifying ligands or modulators of a G-protein Coupled Diadenosine  
 XX Tetraphosphate (AP4A) receptor for e.g. treating hypertension, by  
 XX measuring the binding of AP4A to the receptor in the presence or absence  
 XX of a candidate substance.

XX Claim 1; Page 11; 65pp; English.  
 XX The invention relates to a method for identifying/determining ligands for  
 XX human Diadenosine Tetraphosphate (AP4A) receptor (AP4AR) which is a G-  
 XX protein coupled receptor (GPR56). The method is used for identifying  
 XX ligands, agonists or antagonists of the AP4AR polypeptide. The novel  
 XX substance is useful for the treatment, alleviation and/or prophylaxis of  
 XX an AP4AR-related dysfunction, disorder or disease particularly those  
 XX associated with the cardiovascular system e.g. hypertension or  
 XX vasodilation, regulation of haemostasis, myocardial ischaemia, ischaemic  
 XX preconditioning or cardioprotective activity, central nervous system),  
 XX glucose and insulin metabolism, immunological disorders or disorders of  
 XX genitourinary system. AP4AR polypeptide or gene is also useful as  
 XX vaccines for inducing immunological responses in a mammal. The present  
 XX sequence is human AP4AR cDNA

XX Sequence 2082 BP; 386 A; 707 C; 546 G; 443 T; 0 U; 0 Other;  
 XX  
 XX Query Match 95.5%; Score 21; DB 6; Length 2082;  
 XX Best Local Similarity 100.0%; Pred. No. 5.8;  
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTCGAGTTCTCGATGAGAT 21  
 XX |||||  
 XX DB 186 TTTCGAGTTCTCGATGAGAT 166  
 XX  
 XX RESULT 31  
 XX ABX16439/C  
 XX ID ABX16439 standard; DNA; 2231 BP.  
 XX AC ABX16439;  
 XX DT 15-APR-2003 (first entry)  
 XX XX



DE DNA encoding human SNORF10 receptor.  
 XX  
 XX SNORF10: receptor; human; inflammation; arthritis; autoimmune disease;  
 KW transplant rejection; graft vs. host disease; infection; septicemia;  
 KW AIDS; pain; psychotic disorder; neurological disorder; anxiety;  
 KW depression; locomotor problem; respiratory disorder; asthma; obesity;  
 KW eating disorder; body weight disorder; bulimia; diabetes; anorexia;  
 KW nausea; hypertension; hypotension; vascular disorder; cancer; ulcer;  
 KW cardiovascular disorder; ischemia; stroke; urinary retention;  
 KW sexual disorder; reproductive disorder; circadian rhythm disorder;  
 KW renal disorder; bone disease; osteoporosis; benign prostatic hypertrophy;  
 KW gastrointestinal disorder; nasal congestion; allergy;  
 KW Parkinson's disease; Alzheimer's disease; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX 5'UTR 1..72 /\*tag= a  
 XX CDS 73..2136 /\*tag= b  
 XX /\*product= "SNORF10 receptor"  
 XX 3'UTR 2137..2231 /\*tag= c  
 XX  
 XX US2002151704-A1.  
 XX 17-OCT-2002.  
 XX 22-OCT-2001; 2001US-00011370.  
 XX 05-APR-1999; 99US-00286085.  
 XX  
 XX (BORO/) BOROMSKY B E.  
 XX (OCGOZ/) OCOZALEK K L.  
 XX (KIAM/) KIAM H.  
 XX (PACH/) PATHIRANA M S.  
 XX (SMIT/) SMITH K E.  
 XX  
 XX Borowsky BE, Ogozalek KL, Kyaw H, Pathirana MS, Smith KE;  
 DR MPI: 2003-198335/19.  
 DR P-PSDB; ABG74441.  
 XX  
 PT New recombinant nucleic acid comprising a nucleic acid encoding a  
 PT mammalian SNORF10 receptor, useful for screening antagonist to the  
 PT SNORF10 receptor or as probes to obtain homologous nucleic acids from  
 PT other species.  
 XX  
 XX Claim 2; Fig 1A-D; 19pp; English.  
 XX  
 XX The invention describes a recombinant nucleic acid comprising a nucleic  
 XX acid encoding a mammalian SNORF10 receptor, which hybridizes under  
 XX stringent conditions to a nucleic acid encoding a human SNORF10 receptor  
 XX and having a sequence identical to the sequence of the human SNORF10  
 XX receptor-encoding nucleic acid contained in plasmid pEX2-SNORF10-f. The  
 XX nucleic acid is useful for expressing receptors they encode in  
 XX transfected cells, for screening antagonists to the SNORF10 receptor or  
 XX as probes to obtain homologous nucleic acids from other species and to  
 XX detect the existence of nucleic acids having complementary sequences in  
 XX samples. The protein is useful for treating pathophysiological conditions  
 XX such as chronic and acute inflammation, arthritis, autoimmune disease,  
 XX transplant rejection, graft vs. host disease, bacterial, fungal,  
 XX protozoan and viral infections, septicemia, AIDS, pain, psychotic and  
 XX neurological disorders, anxiety, depression, schizophrenia, dementia,  
 XX mental retardation, memory loss, epilepsy, locomotor problems,  
 XX respiratory disorders, asthma, eating/body weight disorders, obesity,  
 XX bulimia, diabetes, anorexia, nausea, hypertension, hypotension, vascular  
 XX and cardiovascular disorders, ischemia, stroke, cancer, ulcers, urinary  
 XX retention, sexual/reproductive disorders, circadian rhythm disorders,  
 XX renal disorder, bone diseases, osteoporosis, benign prostatic  
 XX hypertrophy, gastrointestinal disorders, nasal congestion, allergies,

CC Parkinson's disease and Alzheimer's disease. This sequence encodes the  
 CC novel human SNORF10 receptor  
 XX  
 XX Sequence 2231 BP; 418 A; 759 C; 587 G; 467 T; 0 U; 0 Other;  
 SQ  
 Query Match 95.5%; Score 21; DB 8; Length 2231;  
 Best Local Similarity 100.0%; Pred. No. 5.8;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGAT 21  
 DB 258 TTGGAGTTCTCGATGAGAT 238  
 RESULT 32  
 AAKS1502/c  
 ID AAKS1502 standard; cDNA; 2713 BP.  
 XX  
 XX AAKS1502;  
 AC  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 47.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200157190-A2.  
 XX 09-AUG-2001.  
 XX 05-FEB-2001; 2001WO-US004098.  
 XX  
 XX 03-FEB-2000; 2000US-00496914.  
 XX 27-APR-2000; 2000US-00560875.  
 XX 20-JUN-2000; 2000US-00598075.  
 XX 19-JUL-2000; 2000US-00620325.  
 XX 01-SEP-2000; 2000US-00654936.  
 XX 15-SEP-2000; 2000US-00663561.  
 XX 20-OCT-2000; 2000US-00693325.  
 XX 30-NOV-2000; 2000US-00728422.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;  
 XX  
 DR MPI: 2001-476283/51.  
 DR P-PSDB; AAM78369.  
 XX  
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful  
 PT in diagnosis and gene therapy.  
 XX  
 XX Claim 1; Page 618-621; 622pp; English.  
 XX  
 XX The invention relates to polynucleotides (AAKS1456-AAKS3435) and the  
 XX encoded polypeptides (AAM78333-AAM80302) that exhibit activity relating to  
 XX cytokine, cell proliferation or cell differentiation or which may induce  
 XX production of other cytokines in other cell populations. The  
 XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 XX peptide therapy. The polypeptides have various cytokine-like activities,  
 XX e.g. stem cell growth factor activity, haematopoietic regulating  
 XX activity, tissue growth factor activity, immunomodulatory activity and  
 XX activin/inhibin activity and may be useful in the diagnosis and/or  
 XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 XX inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111  
 XX (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the  
 CC sequence listing were missing at the time of publication

```
XX Sequence 2713 BP; 489 A; 930 C; 722 G; 571 T; 0 U; 1 Other;
SQ
Query Match 95.5%; Score 21; DB 4; Length 2713;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGGAGTTCTCGATGAGAT 21
Db 186 TTGGAGTTCTCGATGAGAT 166

RESULT 33
ADF70577/c
ID ADF70577 standard; DNA; 2796 BP.
XX
AC ADF70577;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein gene SeqID200.
XX
KM ligand; orphan receptor protein; fusion protein; fluorescent protein;
KM cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KM GFPuv; Enhanced GFP; EGFP; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001501.
XX
PR 22-FEB-2002; 2002JP-00045728.
PR 23-JUL-2002; 2002JP-00213949.
PR 11-OCT-2002; 2002JP-00298237.
XX
PA (TAKE ) TAKEEDA CHEM IND LTD.
XX
PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX
DR WPI; 2003-697654/66.
DR P-PSDB; ADF70475.
XX
PT Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX
PS Example 4; SEQ ID NO 200; 594pp; Japanese.
XX
CC This invention relates to a novel method of identifying ligands to an
CC orphan receptor protein which comprises transforming cells with DNA
CC encoding a fusion protein of the orphan receptor with a fluorescent
CC protein, so that the fusion protein is expressed in the cells (or cell
CC membranes isolated from them) and contacting the cells with the potential
CC ligand to be tested. A suitable fluorescent protein (GFP), for example GFP-1,
CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
CC identification of ligands binding to an orphan receptor protein.
XX
SQ Sequence 2796 BP; 617 A; 865 C; 697 G; 617 T; 0 U; 0 Other;
Qy Query Match 95.5%; Score 21; DB 10; Length 2796;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGGAGTTCTCGATGAGAT 21
Db 186 TTGGAGTTCTCGATGAGAT 166

RESULT 34
```

```
ADA14221/c
ID ADA14221 standard; cDNA; 2816 BP.
XX
AC ADA14221;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human GPR56-3 encoding cDNA SEQ ID NO:5.
XX
KM human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;
KM GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;
KM gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 159..2240
FT /*tag= a
FT /product= "GPR56-3"
XX
PN WO2003068965-A1.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-AU000178.
XX
PR 12-FEB-2002; 2002US-00073054.
XX
PA (GTWO-) G2 THERAPIES LTD.
XX
PI Herzog H, Sutherland RL, Mackay CR, Henhall S;
XX
DR WPI; 2003-689676/65.
DR P-PSDB; ADA14222.
XX
PT New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,
PT useful for preparing a composition for preventing, inhibiting or delaying
PT tumor growth.
XX
PS Example 1; Page 103-106; 129pp; English.
XX
CC The present invention describes a nucleic acid probe for detecting RNA
CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a
CC sample. Also described: (1) detecting a cancer cell in a subject; (2)
CC detecting ovarian cancer or its metastases in a subject; (3) determining
CC an effector memory T cell response in a subject; (4) determining whether
CC or not a subject has been re-infected with an infectious agent; (5)
CC determining the presence of effector memory T cells in a test sample; (6)
CC counting effector memory T cells in a subject; (7) detecting a cancer
CC cell in a subject; (8) reducing or preventing an inflammatory response in
CC a subject; (9) preventing, inhibiting or delaying tumour growth in a
CC subject; and (10) stimulating an immune response in a subject. GPR56 has
CC cytostatic activity, and can be used in gene therapy. The nucleic acid
CC probe is useful for preparing a composition for preventing, inhibiting or
CC delaying tumour growth. The present sequence encodes the human GPCR,
CC designated GPR56-3, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 2816 BP; 517 A; 953 C; 758 G; 588 T; 0 U; 0 Other;
Qy Query Match 95.5%; Score 21; DB 9; Length 2816;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGGAGTTCTCGATGAGAT 21
Db 344 TTGGAGTTCTCGATGAGAT 324

RESULT 35
ADN39449/c
ID ADN39449 standard; cDNA; 2821 BP.
XX
```

AC ADN39449;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:149.  
 XX  
 KM Human; differential expression; cancer; angiogenic disorder;  
 KM fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;  
 KM inflammatory disease; autoimmune disease;  
 KM retinal neovascularization syndrome; scarring; uterine fibroid;  
 KM detection; diagnosis; prognosis; drug screening; drug targeting;  
 KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
 KM vulnery; gene therapy; vaccine; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003042661-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 13-NOV-2002; 2002WO-US036810.  
 XX  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0334934P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0347211P.  
 PR 10-JAN-2002; 2002US-0347349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-0368099P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372246P.  
 PR 15-JUN-2002; 2002US-0386614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397755P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
 XX  
 DR WPI: 2003-468649/44.  
 DR P-PSDB; ADN39450.  
 XX  
 PT Determining the presence or absence of a pathological cell in a patient,  
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
 PT a nucleic acid in a biological sample.  
 XX  
 PS Claim 8; SEQ ID NO 149; 1385bp; English.  
 XX  
 CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
 CC whose expression is upregulated or downregulated in specific cancers or  
 CC other diseases such as angiogenic or fibrotic disorders, and to methods  
 CC of determining the presence or absence of a pathological cell in a  
 CC patient by detecting a nucleic acid at least 80% identical to those of  
 CC the invention or by detecting a polypeptide of the invention. The  
 CC invention also relates to expression vectors and host cells comprising a  
 CC nucleic acid of the invention; antibodies which specifically bind a  
 CC polypeptide of the invention; use of such antibodies for drug targeting;  
 CC and methods of screening for modulators of activity or expression of the  
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
 CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularization syndromes, scarring and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a nucleic acid sequence of the invention.

SO Sequence 2821 BP, 516 A; 948 C; 765 G; 592 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 11; Length 2821;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGAGTTCTCGATGAGAT 21  
 DB 348 TTCGAGTTCTCGATGAGAT 328  
 RESULT 36  
 AAK99413/C  
 ID AAK99413 standard; cDNA; 2822 BP.  
 XX  
 AC AAK99413;  
 XX  
 DT 27-JUN-2002 (first entry)  
 XX  
 DE cDNA of human G protein coupled receptor GPR56.  
 XX  
 KM GPR56; anorectic; G protein-coupled receptor; orphan receptor; obesity;  
 KM appetite control test; transgenic animal; human; chromosome 16q13; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200183558-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 30-APR-2001; 2001WO-GB001865.  
 XX  
 PR 03-MAY-2000; 2000US-0201422P.  
 XX  
 PA (ASTR) ASTRAZENECA AB.  
 PA (ASTR) ASTRAZENECA UK LTD.  
 XX  
 PI Brenand JC, Hart KA;  
 XX  
 DR WPI: 2002-066520/09.  
 XX  
 PT Use of G protein-coupled receptor, GPR56, to identify appetite control  
 PT agent by screening GPR56 agonists or antagonists and selecting active  
 PT agents by subjecting identified compounds to appetite control test  
 PT method.  
 XX  
 PS Claim 6; Page 14-15; 28pp; English.  
 XX  
 CC The invention relates to the use of a G protein-coupled receptor, GPR56,  
 CC for identifying appetite control agents comprising screening for agonists  
 CC and/or antagonists of GPR56 (an orphan receptor), using one or more  
 CC agonists and/or antagonists so identified as test compounds. In one or  
 CC more appetite control test procedures and selecting an active compound  
 CC for use as an appetite control agent. An agonist or antagonist of GPR56  
 CC identified by the method of the invention, is useful as an appetite  
 CC control agent for controlling appetite in an individual. The dominant  
 CC negative mutant of GPR56 is useful for evaluating the role of GPR56 in  
 CC the control of appetite. A transgenic non-human animal containing the  
 CC GPR56 gene is useful for evaluating the effects of test compounds in  
 CC appetite control and obesity. The agonists or antagonists of GPR56 are  
 CC useful as appetite control agents for controlling obesity. AON is also  
 CC useful as an appetite control agent. This polynucleotide sequence  
 CC represents the cDNA of the human G protein-coupled receptor, GPR56, of  
 CC the invention  
 XX  
 SQ Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 6; Length 2822;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGAGTTCTCGATGAGAT 21  
 |||

Db 348 TTCGAGTCTCGATGAGAT 328

RESULT 37  
AB05329/c  
ID ABA05329 standard; DNA; 2822 BP.

AC ABA05329;  
XX  
XX  
DT 27-FEB-2002 (first entry)

XX Human GPR56 encoding DNA.

XX Human; GPR22; anorectic; appetite control agent; GPR; gene;  
KM G protein-coupled receptor; orphan receptor; antisense gene therapy;  
XX mouse; GPR56; ds.

OS Homo sapiens.

PN WO200183550-A2.

XX 08-NOV-2001.

PF 30-APR-2001; 2001WO-GB001874.

XX 03-MAY-2000; 2000US-0201418P.

PA (ASTR ) ASTRAZENECA AB.

XX (ASTR ) ASTRAZENECA UK LTD.

PI Brennard JC, Hart KA;

XX WPI; 2002-066519/09.

PT Identifying appetite control agent for controlling obesity, comprises  
PT screening agonists or antagonists of G protein-coupled receptor, GPR22,  
PT and using them as test compounds in appetite control test procedures.

XX Claim 6; Page 18-19; 21pp; English.

XX The invention relates to identifying an anorectic appetite control agent,  
CC comprising screening for agonists and/or antagonists of G protein-coupled  
CC receptor GPR22 (an orphan receptor), using one or more agonists and/or  
CC antagonists so identified as test compounds in one or more appetite  
CC control procedures and selecting an active compound for use as an  
CC appetite control agent. An antisense oligonucleotide to the GPR22 gene is  
CC also useful for controlling obesity using antisense gene therapy. Note:  
CC The GPR22 encoding cDNA sequence (ABA05328) and encoded protein  
CC (AAM47903) are disclosed, however two DNA sequences described as human  
CC (ABA05328) and mouse (ABA05328) GPR56 are given in the sequence listing  
CC but are not otherwise referred to in the specification

XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 6; Length 2822;

XX Best Local Similarity 100.0%; Pred. No. 5.9; Mismatches 0; Indels 0; Gaps 0;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21

Db 348 TTCGAGTCTCGATGAGAT 328

RESULT 38  
AB242865/c

XX ID AB242865 standard; DNA; 2822 BP.

XX AB242865;

XX 04-MAR-2003 (first entry)

XX Human G protein-coupled receptor TM7XN1/GPR56 DNA SEQ ID NO:517.

KM G protein-coupled receptor, GPCR; antigenic peptide; gene therapy;  
KM G protein-coupled receptor modulator; antibody; immune-related disease;  
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KM immunological-related cell proliferative disease; autoimmune disease;  
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KM psoriasis; anxiety; depression; schizophrenia; multiple sclerosis; pain;  
KM graft versus host disease; Parkinson's disease; memory loss;  
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KM ulcer; gene; ds.

OS Homo sapiens.

PN WO200261087-A2.

XX 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

PI Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX P-PSDB; ABP82015.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (1) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention

XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;

XX Query Match 95.5%; Score 21; DB 8; Length 2822;

XX Best Local Similarity 100.0%; Pred. No. 5.9; Mismatches 0; Indels 0; Gaps 0;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21

Db 348 TTCGAGTCTCGATGAGAT 328

```
RESULT 39
ID ADA14217/c
XX ADA14217 standard; cDNA; 2822 BP.
AC
XX ADA14217;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human GPR56-1 encoding cDNA SEQ ID NO.1.
DE
XX
XX human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;
XX GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;
XX gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 163..2244
XX /tag= a
XX /product= "GPR56-1"
XX
XX MO2003068965-A1.
XX
XX 21-AUG-2003.
XX
XX 12-FEB-2003; 2003WO-AU000178.
XX
XX 12-FEB-2002; 2002US-00073054.
XX
XX (GTWO-) G2 THERAPIES LTD.
XX
XX Herzog H, Sutherland RL, Mackay CR, Henshall S;
XX
XX WPI; 2003-689676/65.
XX P-PSDB; ADA14218.
XX
XX New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,
XX useful for preparing a composition for preventing, inhibiting or delaying
XX tumor growth.
XX
XX Claim 1, Page 88-92; 129pp; English.
XX
XX The present invention describes a nucleic acid probe for detecting RNA
XX encoding a G protein-coupled receptor (GPCR), designated GPR56, in a
XX sample. Also described: (1) detecting a cancer cell in a subject; (2)
XX detecting ovarian cancer or its metastases in a subject; (3) determining
XX an effector memory T cell response in a subject; (4) determining whether
XX or not a subject has been re-infected with an infectious agent; (5)
XX determining the presence of effector memory T cells in a test sample; (6)
XX counting effector memory T cells in a subject; (7) detecting a cancer
XX cell in a subject; (8) reducing or preventing an inflammatory response in
XX a subject; (9) preventing, inhibiting or delaying tumour growth in a
XX subject; and (10) stimulating an immune response in a subject. GPR56 has
XX cytotaxic activity, and can be used in gene therapy. The nucleic acid
XX probe is useful for preparing a composition for preventing, inhibiting or
XX delaying tumour growth. The present sequence encodes the human GPCR,
XX designated GPR56-1, which is used in the exemplification of the present
XX invention.
XX
XX Sequence 2822 BP; 516 A; 949 C; 765 G; 592 T; 0 U; 0 Other;
SQ
XX
XX Query Match 95.5%; Score 21; DB 9; Length 2822;
XX Best Local Similarity 100.0%; Pred. No. 5.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY
XX 1 TTCGAGTCTCGATGAGAT 21
XX |||||
XX 348 TTCGAGTCTCGATGAGAT 328
XX
XX RESULT 40
XX AAX25359/c
XX ID AAX25359 standard; cDNA; 2834 BP.
XX
XX AAX25359 standard; cDNA; 2834 BP.
```

```
XX
XX AAX25359;
AC
XX 19-JUL-1999 (first entry)
XX
XX Human G protein coupled receptor TSR32 cDNA.
DE
XX
XX TSR32; G protein coupled receptor; thyroid; human; Bardet Biedl syndrome;
XX ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 169..2250
XX /tag= a
XX
XX MO915551-A1.
XX
XX 01-APR-1999.
XX
XX 24-SEP-1998; 98WO-AU000805.
XX
XX 24-SEP-1997; 97AU-0009386.
XX
XX (GARV-) GARVAN INST MEDICAL RES.
XX
XX Herzog H;
XX
XX WPI; 1999-244386/20.
XX P-PSDB; AAY05730.
XX
XX New G-protein-coupled receptor designated TSR32.
XX
XX Claim 5; 10-11; 23pp; English.
XX
XX This is the nucleotide sequence of an isolated polynucleotide, the coding
XX region of which is also claimed, encoding a new human G protein coupled
XX receptor, termed TSR32 (see AAY05730), which is a member of the secretin
XX receptor family. TSR32 is expressed in many tissue types, with highest
XX expression in the thyroid gland, suggesting that TSR32 has important
XX functions in metabolic regulation throughout the body via the thyroid
XX gland. TSR32 cDNA was isolated from a human heart cDNA library using a
XX 466 bp fragment that had itself identified using degenerate
XX oligonucleotides based on conserved regions of the human glucagon-like
XX peptide receptor family. The invention provides TSR32 polypeptides,
XX polynucleotides, a vector, host cells, an antibody and a non-human
XX transgenic animal, as well as a method for detecting agonists or
XX antagonists of TSR32, oligonucleotide or polynucleotide probes, an
XX antisense polynucleotide, and a method of producing TSR32 or its
XX polypeptides by culturing the host cells. The TSR32 protein, its agonists
XX and antagonists can be used to regulate thyroid functions in growth,
XX development and metabolic activity. The gene for TSR32 has been mapped to
XX chromosome 16q31, where Bardet Biedl syndrome, an autosomal recessive
XX disorder, has been linked
XX
XX Sequence 2834 BP; 520 A; 951 C; 767 G; 596 T; 0 U; 0 Other;
SQ
XX
XX Query Match 95.5%; Score 21; DB 2; Length 2834;
XX Best Local Similarity 100.0%; Pred. No. 5.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY
XX 1 TTCGAGTCTCGATGAGAT 21
XX |||||
XX 354 TTCGAGTCTCGATGAGAT 334
XX
XX RESULT 41
XX AAX35743/c
XX ID AAX35743 standard; cDNA; 3563 BP.
XX
XX AAX35743;
AC
XX
XX 09-JUL-1999 (first entry)
```

XX DE cDNA encoding a protein identified by the signal sequence trap method.  
 XX XX  
 KW Signal sequence trap method; SST method; immunisation; inhibition;  
 KW infection; allergy; cancer; regulation; tissue formation; tissue repair;  
 KW actin activity; inhibin activity; chemokine activity;  
 KW cytokine activity; blood coagulation regulation; agonist; antagonist;  
 KW metabolic disorder; hormonal disorder; immune disorder;  
 KW severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;  
 KW ss.  
 XX OS Homo sapiens.  
 XX OS MO9918126-A1.  
 XX PN 15-APR-1999.  
 XX PD 06-OCT-1998; 98MO-JP004514.  
 XX PF 07-OCT-1997; 97JP-00274674.  
 XX PR (ONOV ) ONO PHARM CO LTD.  
 XX PA Fukushima D, Shibayama S, Tada H;  
 XX PI WPI; 1999-277254/23.  
 XX DR P-PSDB; AAY02382.  
 XX PT Polypeptides identified by the signal sequence trap method from a human  
 XX PT cDNA library.  
 XX PS Claim 5; Page 233-238; 281pp; Japanese.  
 XX PS AX35694-X35747 represent cDNA sequences that encode novel polypeptides  
 XX CC (AAY02358-84) which are identified from a human placental cDNA library by  
 CC the signal sequence trap (SST) method. The polypeptides have a broad  
 CC range of physiological activity, including immunisation against and  
 CC inhibition of infections, allergies and cancer; regulation of tissue  
 CC formation and repair; actin/inhibin activity; chemokine/cytokine  
 CC activity; blood coagulation regulation; and receptor/ligand agonist or  
 CC antagonist activity. The polypeptides can be used for prevention and  
 CC treatment of disorders including infections by bacteria, yeasts and  
 CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;  
 CC immune disorders (including severe combined immunodeficiency (SCID) and  
 CC AIDS; thrombosis; cancer; and traumatic or surgical wounds  
 CC XX  
 SQ Sequence 3563 BP; 689 A; 1163 C; 934 G; 777 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 2; Length 3563;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGAT 21  
 Db 228 TTGGAGTTCTCGATGAGAT 208  
 RESULT 42  
 ID AAA09348/C  
 XX AAA09348 standard; DNA; 3632 BP.  
 XX AC AAA09348;  
 XX XX  
 XX DT 10-AUG-2000 (first entry)  
 XX DE G protein-coupled receptor protein 1 coding sequence.  
 XX XX  
 KW GPCR-1; G protein-coupled receptor protein; antipneumatic; antineumatic;  
 KW epidiymis-specific seven transmembrane receptor; HB6; immunosuppressive;  
 KW antiaerthmatic; antienemic; antiaertherosclerotic; antihypoid; cyotetic;  
 KW hepatotropic; dermatological; anti-inflammatory; antipain; thymimetic;  
 KW haemostatic; virucide; hepatotropic; osteopathic; antiparasttic;  
 KW immunostimulant; ss.

XX OS Homo sapiens.  
 XX XX  
 XX FH Key Location/Qualifiers  
 XX FT CDS 96..2177  
 XX FT /\*tag= a  
 XX PN WO200020590-A2.  
 XX PD 13-APR-2000.  
 XX PF 06-OCT-1999; 99MO-US023317.  
 XX PR 06-OCT-1998; 98US-00167219.  
 XX PR 06-OCT-1998; 98US-0172211P.  
 XX PR 11-MAY-1999; 99US-0133585P.  
 XX PA (INCYTE-) INCYTE PHARM INC.  
 XX XX  
 XX PI Tang YT, Yue H, Lal P, Bandman O, Au-Young J, Reddy R;  
 XX PI Corley NC, Guegler KJ, Gorgone GA, Baughn MR, Azimzal Y;  
 XX XX  
 XX DR WPI; 2000-338934/28.  
 XX DR P-PSDB; AAY92362.  
 XX XX  
 XX PT Novel human G-protein coupled receptor proteins used in the diagnosis,  
 XX PT treatment and prevention of nervous system disorders,  
 XX PT autoimmune/inflammatory disorders, and cell proliferative disorders such  
 XX PT as cancer.  
 XX PS Claim 9; Page 75; 84pp; English.  
 XX PS This sequence encodes human G-protein coupled receptor protein (GCRP) 1,  
 XX CC which has similarity with human epidiymis-specific seven transmembrane  
 CC receptor HB6. The GCRP polypeptides, polynucleotides, antibodies,  
 CC antagonists and agonists may be administered to human patients for the  
 CC diagnosis, treatment and prevention of nervous system disorders (e.g.  
 CC epilepsy, stroke, neoplasms, Alzheimer's disease), autoimmune or  
 CC inflammatory disorders, complications of cancer, hemodialysis and  
 CC extracorporeal circulation, and cell proliferative disorders. They are  
 CC also used to treat or prevent disorders associated with decreased or  
 CC increased expression or activity of GCRP  
 CC XX  
 SQ Sequence 3632 BP; 700 A; 1187 C; 963 G; 782 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 3; Length 3632;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGAGTTCTCGATGAGAT 21  
 Db 281 TTGGAGTTCTCGATGAGAT 261  
 RESULT 43  
 ID AAF28360/C  
 XX AAF28360 standard; CDNA; 3686 BP.  
 XX AC AAF28360;  
 XX XX  
 XX DT 02-APR-2001 (first entry)  
 XX DE Human seven transmembrane receptor protein cDNA.  
 XX XX  
 KW Human; BBSR; Bardet-Biedl Syndrome Region; seven transmembrane receptor;  
 KW antidiabetic; anorectic; ophthalmological; antiinflammatory; noctropic;  
 KW cardiac; nephrotropic; gene therapy; chromosome 16;  
 KW retinal degeneration; hypogentitalism; polydactyly; brachydactyly;  
 KW obesity; mental retardation; renal disorder; diabetes;  
 KW cardiovascular disorder; ss.  
 XX XX  
 XX OS Homo sapiens.



PN WO200100825-A2.  
 XX  
 PD 04-JUN-2001.  
 XX  
 XX 22-JUN-2000; 2000WO-US017375.  
 XX  
 PR 30-JUN-1999; 99US-0141753P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Duhi D, Gorman SW;  
 XX  
 DR WPI; 2001-123009/13.  
 DR P-PSDB; AAB61166.  
 XX  
 PT New human chromosome 15 and 16 Bardet-Biedl Syndrome Region polypeptide  
 PT and polynucleotide for diagnosis and treatment of obesity, retinal  
 PT degeneration, mental retardation, nervous system, heart and kidney  
 PT disorders.  
 XX  
 PS Claim 2; Fig 5; 51pp; English.  
 XX  
 CC The present sequence is one of five novel Bardet-Biedl Syndrome Region  
 CC (BBSR) polynucleotides that map to human chromosome 15 or 16. BBSR  
 CC polynucleotides, polypeptides and anti-BBSR antibodies are useful for  
 CC treating a BBSR protein-modulated disorder in a subject. An antibody that  
 CC specifically binds to a BBSR protein is useful for diagnosing a BBSR  
 CC protein-modulated disorder. BBSR protein-modulated disorders include  
 CC Bardet-Biedl syndrome, retinal degeneration including retinitis  
 CC pigmentosa, hypogonadism, polydactyly, brachydactyly, obesity, mental  
 CC retardation, renal abnormalities, diabetes and cardiovascular  
 CC abnormalities. BBSR polypeptides are also useful for screening  
 CC combinatorial libraries to identify agonist or antagonists. Antibodies  
 CC against BBSR polypeptides are useful for affinity chromatography, for  
 CC distinguishing BBSR polypeptides and for inhibiting or modulating an  
 CC activity or biological effect or a disorder associated with the BBSR  
 CC proteins  
 CC  
 SQ Sequence 3686 BP; 737 A; 1192 C; 952 G; 803 T; 0 U; 2 Other;  
 Query Match 95.5%; Score 21; DB 4; Length 3686;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 TTCCGAGTCTCGATGAGAT 21  
 Db 318 TTCCGAGTCTCGATGAGAT 298  
 RESULT 44  
 ADL26765/c  
 ID ADL26765 standard; cDNA; 3702 BP.  
 XX  
 AC ADL26765;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human GPR56 encoding cDNA SEQ ID NO:19.  
 XX  
 KW ovarian cancer; ovarian cancer-associated transcript; cytostatic;  
 KW gene therapy; human; GPR56; chromosome 16; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 159..2240  
 FT /tag= a  
 FT /product= "GPR56"  
 XX  
 PN WO2004022778-A1.  
 XX  
 PD 18-MAR-2004.  
 XX

PF 05-SEP-2003; 2003WO-AU001166.  
 XX  
 PR 05-SEP-2002; 2002AU-00951346.  
 XX  
 XX (GARV-) GARVAN INST MEDICAL RES.  
 XX  
 PI Sutherland R, Henshall S, O'Brien P;  
 XX  
 DR WPI; 2004-315574/29.  
 DR P-PSDB; ADL26766.  
 XX  
 PT Use of genes and proteins for diagnosing ovarian cancer and/or a  
 PT likelihood for survival or recurrence of the disease.  
 PS  
 PS Claim 2; SEQ ID NO 19; 447pp; English.  
 XX  
 CC The present invention describes a method for the use of genes and  
 CC proteins for diagnosing ovarian cancer and/or a likelihood for survival  
 CC or recurrence of the disease, where the expression of genes and proteins  
 CC is up-regulated and down-regulated or associated with the occurrence or  
 CC recurrence of a specific cancer sub-type. Also described: (1) detecting  
 CC an ovarian cancer-associated transcript in a biological sample; (2)  
 CC diagnosing an ovarian cancer in a human or animal subject being tested;  
 CC (3) detecting an ovarian cancer-associated polypeptide in a biological  
 CC sample; (4) monitoring the efficacy of a therapeutic treatment of ovarian  
 CC cancer; (5) determining the likelihood of survival of a subject suffering  
 CC from an ovarian cancer; and (6) an assay device for use in the diagnosis  
 CC or prognosis of ovarian cancer comprising polynucleotides or antibodies  
 CC immobilised to a solid phase, where each of the polynucleotides consists  
 CC of a gene given in the specification and each of the antibodies binds to  
 CC a polypeptide also given in the specification; and identifying a  
 CC candidate compound for the treatment of ovarian cancer. An ovarian cancer  
 CC -associated sequence has cytostatic activity, and can be used in gene  
 CC therapy. An ovarian cancer-associated polynucleotide, vector, polypeptide  
 CC or antibody can be used for the diagnosis or prognosis of ovarian cancer  
 CC or for the preparation of a medicament for the treatment of ovarian  
 CC cancer. The ovarian cancer that is diagnosed is an epithelial ovarian  
 CC cancer selected from serous ovarian cancer, non-invasive ovarian cancer,  
 CC mixed phenotype ovarian cancer, mucinous ovarian cancer, endometrial  
 CC ovarian cancer, clear cell ovarian cancer, papillary serous ovarian  
 CC cancer, Brenner cell or undifferentiated adenocarcinoma. The present  
 CC sequence encodes human GPR56, which is located on chromosome 16 and is  
 CC used in the exemplification of the present invention.  
 CC  
 SQ Sequence 3702 BP; 713 A; 1206 C; 973 G; 810 T; 0 U; 0 Other;  
 Query Match 95.5%; Score 21; DB 12; Length 3702;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 TTCCGAGTCTCGATGAGAT 21  
 Db 344 TTCCGAGTCTCGATGAGAT 324  
 RESULT 45  
 ADN95755/c  
 ID ADN95755 standard; DNA; 3710 BP.  
 XX  
 AC ADN95755;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human BEC/LBC-related gene sequence SeqID679.  
 XX  
 KW growth; differentiation; blood endothelial cell; BEC;  
 KW lymphatic endothelial cell; LBC; hereditary lymphedema; VEGFR-3;  
 KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;  
 KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;  
 KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;  
 KW human.  
 XX  
 OS Homo sapiens.  
 OS

```

XX  MO2003080640-A1.
XX
XX  02-OCT-2003.
XX
XX  07-MAR-2003; 2003WO-US006900.
XX
XX  07-MAR-2002; 2002US-0363019P.
XX
XX  (LUDW-) LUDWIG INST CANCER RES.
XX  (LICN ) LICENTIA LTD.
XX
XX  Alltalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX
XX  WPI: 2003-876899/81.
XX  P-PSDB; ADN95754.
XX
XX  Example 1; SEQ ID NO 679; 176pp; English.
XX
XX  This invention relates to a method of differentially modulating the
XX  growth or differentiation of blood endothelial cells (BEC) or lymphatic
XX  endothelial cells (LEC) comprises contacting endothelial cells with a
XX  composition comprising an agent that differentially modulates blood or
XX  lymphatic endothelial cells. Treating hereditary lymphoedema comprises
XX  identifying a human subject with lymphoedema and with a mutation in at
XX  least one allele of a gene encoding a LEC protein, where the mutation
XX  correlates with lymphoedema in human subjects, and with the proviso that
XX  the LEC protein is not VEGFR-3; and administering to the subject a
XX  composition comprising a lymphatic growth agent selected from VEGF-C or
XX  VEGF-D polypeptides and polynucleotides. The invention may be useful for
XX  the development of compounds with an antiangiogenic, cytostatic,
XX  vasorelaxant or antiinflammatory activity or for gene therapy. The method
XX  is useful in modulating the growth or differentiation of blood
XX  endothelial cells or lymphatic endothelial cells, in treating hereditary
XX  lymphoedema, in screening for an endothelial cell disorder or
XX  predisposition to the disorder or in monitoring the efficacy or toxicity
XX  of a drug on endothelial cells. The agent is useful in manufacturing a
XX  medicament for the differential modulation of blood vessel endothelial
XX  cell or lymphatic vessel endothelial cell growth or differentiation. The
XX  lymphatic growth agent may also be used in manufacturing a medicament for
XX  the treatment of hereditary lymphoedema resulting from a mutation in a
XX  LEC gene or of other diseases involving the lymphatic vessels, such as
XX  various inflammatory diseases and cancer metastasis via the lymphatic
XX  system. The present sequence is that of a human LEC/BEC differentially
XX  expressed gene which is related to the method of the invention. Note: This
XX  sequence does not appear in the specification but was obtained by the
XX  index using the source data given in table 14 of the specification.
XX
XX  Sequence 3710 BP; 714 A; 1208 C; 978 G; 810 T; 0 U; 0 Other;
SQ
Query Match          95.5%; Score 21; DB 11; Length 3710;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 TTCCGAGTTCGATGAGAT 21
    |||||
DB  353 TTCCGAGTTCGATGAGAT 333

```

```

KM  signal transduction activator; bone disease; hypertension; renal failure;
KM  heart failure; hyperthyroidism; hyperparathyroidism; carcinoma;
KM  sarcoidosis; pancreatitis; stress; high blood pressure;
KM  immune depression; periodontal disease; neurodegenerative disease;
KM  multiple sclerosis; Alzheimer's disease; Parkinson's disease;
KM  schizophrenia; manic depression; stroke; rheumatoid arthritis;
KM  male fertility; spermatogenesis stimulation; pregnancy regulation;
KM  prostate cancer; ss.
XX
XX  Homo sapiens.
XX
XX  Key      Location/Qualifiers
XX  CDS      190..2271
XX           /*tag= a
XX           /product= "zsig56"
XX           /length= 264
XX           /*tag= b
XX           mat_peptide 265..2258
XX           /*tag= c
XX
XX  WO200034473-A2.
XX
XX  15-JUN-2000.
XX
XX  02-DEC-1999; 99WO-US028492.
XX
XX  10-DEC-1998; 98US-00208691.
XX
XX  (ZYMO ) ZYMOGENETICS INC.
XX
XX  Shepard PO, Elsworth JL;
XX
XX  WPI: 2000-442164/38.
XX  P-PSDB; AAB01246.
XX
XX  Novel G-protein coupled receptor zsig56 useful for treating hypertension,
XX  hyper and hypothyroidism, inflammation, gout, carcinoma, pancreatitis,
XX  Alzheimer's disease and Parkinson's disease, renal and heart failure.
XX
XX  Claim 2; Page 104-109; 121pp; English.
XX
XX  The present sequence encodes a seven transmembrane domain receptor
XX  designated zsig56. The full length nucleotide sequence was obtained from
XX  a human retina library. zsig56 polypeptides, nucleic acid, agonists
XX  and/or antagonists may be used to treat a wide range of disorders
XX  including certain bone diseases, hypertension, renal failure, gout,
XX  congestive heart failure, hyperthyroidism, hyperparathyroidism, certain
XX  carcinomas, sarcoidosis and pancreatitis. They can be used to treat
XX  disorders associated with changes in ion or electrolyte homeostasis, and
XX  stress induced disorders such as high blood pressure, heart failure,
XX  immune depression and periodontal disease. They may be used to treat
XX  neurodegenerative diseases, including multiple sclerosis, Alzheimer's
XX  disease and Parkinson's disease, schizophrenia and manic depression, and
XX  to repair nerve tissue following damage due to strokes and brain and
XX  spinal injuries. Inflammatory disorders such as rheumatoid arthritis can
XX  also be treated. zsig56 is expressed in tissues associated with
XX  reproduction, i.e. the testis, prostate and placenta, and may be used to
XX  treat male fertility by stimulating spermatogenesis and to regulate
XX  gestation and birth. zsig56 may be useful as a marker or therapeutic
XX  agent in the treatment of prostate cancer
XX
XX  Sequence 3711 BP; 710 A; 1217 C; 971 G; 813 T; 0 U; 0 Other;
SQ
Query Match          95.5%; Score 21; DB 3; Length 3711;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 TTCCGAGTTCGATGAGAT 21
    |||||
DB  375 TTCCGAGTTCGATGAGAT 355

```

RESULT 47

AAD57428/c  
 ID AAD57428 standard; DNA; 3711 BP.  
 XX  
 AC AAD57428;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human TM7XN1 protein.  
 XX  
 KM Human; therapy; renal carcinoma; non-melanoma tumour; GPCR; astrocytoma;  
 KM brain tumour; adenocarcinoma; G-protein coupled receptor; glioblastoma;  
 KM tumour target protein; TM7XN1; cytotoxic; receptor; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 168..2249  
 FT /tag= a  
 FT /product= "Human TM7XN1 protein"  
 XX  
 PN WO2003057148-A2.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 23-DEC-2002; 2002WO-US041419.  
 XX  
 PR 27-DEC-2001; 2001US-0343422P.  
 XX  
 PA (AGYT-) AGY THERAPEUTICS INC.  
 PA (GONZ/) GONZALEZ-ZULUETA M.  
 XX  
 PI Gonzalez-Zulueta M, Mueller S, Foehr E, Chin D;  
 XX  
 DR WPI; 2003-598311/56.  
 DR P-PSDB; AAB38135.  
 XX  
 PT Treating brain tumor e.g., astrocytoma, or adenocarcinoma, non-melanoma  
 PT tumor and renal carcinoma by administering a compound that specifically  
 PT binds a TM7XN1 protein, and is conjugated to one or more cytotoxic  
 PT groups.  
 XX  
 PS Example 1; Page 66-70; 73pp; English.  
 XX  
 CC The invention relates to a method of treating brain tumour, renal  
 CC carcinoma, non-melanoma tumour and adenocarcinoma. The method involves  
 CC administering a compound that specifically binds a GPCR (G-protein  
 CC coupled receptor) tumour target protein, TM7XN1 where the compound is  
 CC conjugated to one or more cytotoxic groups. The method is useful for  
 CC treating brain tumour (e.g. astrocytoma preferably glioblastoma),  
 CC adenocarcinoma, non-melanoma tumour and renal carcinoma. The method is  
 CC useful for developing biologically active agents that modulate activity  
 CC of brain tumour target gene or gene product. The present sequence is  
 CC human TM7XN1 DNA  
 CC  
 SQ Sequence 3711 BP; 715 A; 1208 C; 978 G; 810 T; 0 U; 0 Other;  
 XX  
 QY Query Match 95.5%; Score 21; DB 9; Length 3711;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 TTCGAGTCTCGATGAGAT 21  
 353 TTCGAGTCTCGATGAGAT 333  
 XX  
 RESULT 48  
 ID ADA14219/c  
 XX ADA14219 standard; cDNA; 3711 BP.  
 AC ADA14219;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX

DE Human GPR56-2 encoding cDNA SEQ ID NO:3.  
 XX  
 XX human; nucleic acid probe; detection; G protein-coupled receptor; GPCR;  
 KM GPR56; cancer; ovarian cancer; metastasis; tumour; cytostatic;  
 KM gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 168..2249  
 FT /tag= a  
 FT /product= "GPR56-2"  
 XX  
 PN WO2003068965-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 12-FEB-2003; 2003WO-AU000178.  
 XX  
 PR 12-FEB-2002; 2002US-00073054.  
 XX  
 PA (GW0-) G2 THERAPIES LTD.  
 XX  
 PI Herzog H, Sutherland RL, Mackay CR, Henshall S;  
 XX  
 DR WPI; 2003-689676/65.  
 DR P-PSDB; ADA14220.  
 XX  
 PT New nucleic acid probe for detecting RNA encoding a GPR56 polypeptide,  
 PT useful for preparing a composition for preventing, inhibiting or delaying  
 PT tumor growth.  
 XX  
 PS Example 1; Page 95-99; 129pp; English.  
 XX  
 CC The present invention describes a nucleic acid probe for detecting RNA  
 CC encoding a G protein-coupled receptor (GPCR), designated GPR56, in a  
 CC sample. Also described: (1) detecting a cancer cell in a subject; (2)  
 CC detecting ovarian cancer or its metastases in a subject; (3) determining  
 CC an effector memory T cell response in a subject; (4) determining whether  
 CC or not a subject has been re-infected with an infectious agent; (5)  
 CC determining the presence of effector memory T cells in a test sample; (6)  
 CC counting effector memory T cells in a subject; (7) detecting a cancer  
 CC cell in a subject; (8) reducing or preventing an inflammatory response in  
 CC a subject; (9) preventing, inhibiting or delaying tumour growth in a  
 CC subject; and (10) stimulating an immune response in a subject. GPR56 has  
 CC cytostatic activity, and can be used in gene therapy. The nucleic acid  
 CC probe is useful for preparing a composition for preventing, inhibiting or  
 CC delaying tumour growth. The present sequence encodes the human GPCR,  
 CC designated GPR56-2, which is used in the exemplification of the present  
 CC invention.  
 CC  
 SQ Sequence 3711 BP; 715 A; 1208 C; 978 G; 810 T; 0 U; 0 Other;  
 XX  
 QY Query Match 95.5%; Score 21; DB 9; Length 3711;  
 Best Local Similarity 100.0%; Pred. No. 6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 TTCGAGTCTCGATGAGAT 21  
 353 TTCGAGTCTCGATGAGAT 333  
 XX  
 RESULT 49  
 ID AAK94597/c  
 XX AAK94597 standard; cDNA; 3748 BP.  
 AC AAK94597;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human full-length cDNA, SEQ ID NO: 3537.  
 DE Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
 XX

```

XX Homo sapiens.
OS
XX EP130094-A2.
PN
XX 05-SEP-2001.
PD
XX 07-JUL-2000; 2000EP-00114089.
PF
XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
DR WPI; 2001-524255/58.
DR P-PSDB; AAW93662.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
PS
XX Claim 8; SEQ ID NO 3537; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesized by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence data is a full length human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in CD-ROM format directly
CC from EPO
XX
SQ Sequence 3748 BP; 709 A; 1219 C; 1004 G; 816 T; 0 U; 0 Other;

Query Match          95.5%; Score 21; DB 4; Length 3748;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21
Db 430 TTCGAGTTCGATGAGAT 410

RESULT 50
ADL31504/c
ID ADL31504 standard; cDNA; 3748 BP.
XX
AC ADL31504;
XX
DT 20-MAY-2004 (first entry)
XX
DE Full length human cDNA clone SeqID 3537.
XX
KM human; medicine; signal transduction; glycoprotein; transcription;
KM oligo-capping method; ss; gene.
XX
XX Homo sapiens.
OS
XX EP1396543-A2.
PN
XX 10-MAR-2004.
PD
XX 07-JUL-2000; 2003EP-00025638.
PF
XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR

```

```

PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PA Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2004-204755/20.
DR P-PSDB; ADL31505.
DR
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
PT
XX Example 1; SEQ ID NO 3537; 1340pp; English.
PS
XX This invention relates to a novel primers useful for synthesizing full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction,
XX glycoproteins and transcription. The present invention describes a method
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
XX ends using the oligo-capping method. This polynucleotide sequence is a
XX full length human cDNA clone of the invention.
XX
SQ Sequence 3748 BP; 709 A; 1219 C; 1004 G; 816 T; 0 U; 0 Other;

Query Match          95.5%; Score 21; DB 12; Length 3748;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21
Db 430 TTCGAGTTCGATGAGAT 410

Search completed: February 2, 2005, 00:06:13
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-073-054-14

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Scoring table: IDENTITY\_NUC  
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Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 500 summaries

Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsa1:  
9: gb\_gsa2:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	95.5	315	2	BE938539 RCO-TN008
2	21	95.5	383	4	BM151906 TCBAPE11
3	21	95.5	453	4	BM193168 TCBAPE10
4	21	95.5	464	2	AM844829 RC3-CN005
5	21	95.5	474	2	BE245815 TCBAPE11
6	21	95.5	475	2	BF841366 RC2-HT107
7	21	95.5	496	5	BE475238 DKFZP686N
8	21	95.5	512	2	BE244425 TCBAPE16
9	21	95.5	515	2	BE391006 601285614
10	21	95.5	520	2	BE244892 TCBAPE127
11	21	95.5	522	2	BE243851 TCBAPE16
12	21	95.5	523	7	CN337098 170004706
13	21	95.5	524	2	BE019655
14	21	95.5	527	2	AM837046 QV1-LT003
15	21	95.5	531	2	BE246307 TCBAPE16
16	21	95.5	532	5	BE475095 DKFZP686J
17	21	95.5	535	5	BE475505 DKFZP686H
18	21	95.5	542	5	BE475102 DKFZP686J
19	21	95.5	559	6	CA390929 csl16c02.
20	21	95.5	568	2	BE206268 ba96e12.x
21	21	95.5	570	1	AL707342 DKFZP686C
22	21	95.5	573	1	AL598371 DKFZP313A
23	21	95.5	583	5	BE475118 DKFZP686K
24	21	95.5	601	5	BE506361 DKFZP686N

25	21	95.5	607	5	BK485768
26	21	95.5	613	4	BG819058 602781132
27	21	95.5	618	4	BG819937 602782040
28	21	95.5	636	4	BI766999 603054091
29	21	95.5	643	4	BI850146
30	21	95.5	649	1	AL046540
31	21	95.5	682	4	BG718773
32	21	95.5	697	4	BI666902 603291647
33	21	95.5	728	1	AL133937 DKFZP761P
34	21	95.5	732	4	BI767127 603054191
35	21	95.5	741	4	BI464202 603203303
36	21	95.5	752	4	BG910316
37	21	95.5	755	7	CN337099 170005315
38	21	95.5	757	4	BG705518 60286543
39	21	95.5	761	4	BG536985 60265045
40	21	95.5	773	4	BI907794 603066045
41	21	95.5	774	7	CF995022 AGENCOURT
42	21	95.5	777	5	BQ433220 AGENCOURT
43	21	95.5	785	4	BI553947 603193818
44	21	95.5	806	4	BI601981 603243977
45	21	95.5	811	7	CF995140 AGENCOURT
46	21	95.5	817	6	CD246163 AGENCOURT
47	21	95.5	827	6	CB987979 AGENCOURT
48	21	95.5	835	2	BI25765 AGENCOURT
49	21	95.5	840	1	AL598478 AGENCOURT
50	21	95.5	854	2	BE893273 AGENCOURT
51	21	95.5	865	4	BI550216 603193821
52	21	95.5	872	4	BI559738 603252621
53	21	95.5	889	5	BU156180 AGENCOURT
54	21	95.5	908	5	BQ432053 AGENCOURT
55	21	95.5	930	5	BU171654 AGENCOURT
56	21	95.5	941	5	BK384045 AGENCOURT
57	21	95.5	958	4	BF345820 AGENCOURT
58	21	95.5	971	5	BK417949 AGENCOURT
59	21	95.5	981	5	BK339034 AGENCOURT
60	21	95.5	1042	4	BM551558 AGENCOURT
61	21	95.5	1077	4	BM562072 AGENCOURT
62	21	95.5	1090	4	BG818281 AGENCOURT
63	21	95.5	1112	4	BM452153 AGENCOURT
64	21	95.5	1118	5	BK440894 AGENCOURT
65	21	95.5	1135	2	BE744756 601573171
66	21	95.5	1137	1	AL553171 AGENCOURT
67	21	95.5	1355	5	B0068139 AGENCOURT
68	21	95.5	3835	3	BC013207 Homo sapi
69	20	90.9	540	7	CR651011
70	19.4	88.2	212	1	AI559387
71	19.4	88.2	317	4	BM193164 TCBAPE10
72	19.4	88.2	735	2	BE280709 601155990
73	18.8	85.5	218	9	CC661759 OCOAN95TV
74	18.8	85.5	639	6	CB212094 OGBRK55TV
75	18.8	85.5	768	9	CG3177004 AGENCOURT
76	18.8	85.5	843	9	CG722513 OGDH081TH
77	18.8	85.5	881	9	CG254830 OGC2CO8TV
78	18.8	85.5	915	9	CG279152 OGVF86TV
79	18.8	85.5	979	9	CG259010 OGDH081TV
80	18.8	85.5	980	9	CG722523 OGDH081TV
81	18.4	83.6	627	7	CF574369 MGS4114E0
82	17.8	80.9	241	5	BE256984 AGENCOURT
83	17.8	80.9	444	4	BG713095 AGENCOURT
84	17.8	80.9	492	7	CF428016 PH1_12.H1
85	17.8	80.9	516	5	BP123044 BP123044
86	17.8	80.9	516	5	BP124112 BP124112
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88	17.8	80.9	539	4	BE132254 SD25965.5
89	17.8	80.9	539	4	BE132254 SD25965.5
90	17.8	80.9	539	4	BE132254 SD25965.5
91	17.8	80.9	539	4	BE132254 SD25965.5
92	17.8	80.9	539	4	BE132254 SD25965.5
93	17.8	80.9	539	4	BE132254 SD25965.5
94	17.8	80.9	539	4	BE132254 SD25965.5
95	17.8	80.9	539	4	BE132254 SD25965.5
96	17.8	80.9	539	4	BE132254 SD25965.5
97	17.8	80.9	539	4	BE132254 SD25965.5







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C 390 17.4 79.1 1155 6 CA276199 SCCSD109
C 391 17.2 78.2 196 2 BB344481 BB344481
C 392 17.2 78.2 279 7 CN846540 PG07014H1
C 393 17.2 78.2 300 1 AV180575 AV180575
C 394 17.2 78.2 308 1 AA307607 AA307607
C 395 17.2 78.2 435 8 BH818689 BH818689
C 396 17.2 78.2 474 2 AM624352 EST322297
C 397 17.2 78.2 479 7 M88858 M88858
C 398 17.2 78.2 480 1 AJ472025 AJ472025
C 399 17.2 78.2 484 2 BB859348 BB859348
C 400 17.2 78.2 491 8 CP934648 CP934648
C 401 17.2 78.2 497 8 AL332446 AL332446
C 402 17.2 78.2 539 6 CB395914 CB395914
C 403 17.2 78.2 540 1 AJ472026 AJ472026
C 404 17.2 78.2 572 6 CB399836 CB399836
C 405 17.2 78.2 576 6 BJ759712 BJ759712
C 406 17.2 78.2 619 9 CC974347 CC974347
C 407 17.2 78.2 623 1 AU060682 AU060682
C 408 17.2 78.2 643 4 BM510797 BM510797
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C 417 17.2 78.2 759 9 CL675919 PR10116a
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C 444 17.2 77.3 144 1 AL827816 AL827816
C 445 16.8 76.4 260 1 AL827811 AL827811
C 446 16.8 76.4 284 4 BBS44525 BBS44525
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C 449 16.8 76.4 394 4 BJ275455 BJ275455
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C 473 16.8 76.4 668 6 CD873314 CD873314
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C 484 16.8 76.4 806 5 BP119782 BP119782
C 485 16.8 76.4 832 6 CD656280 CD656280
C 486 16.8 76.4 847 8 AO329512 AO329512
C 487 16.8 76.4 916 9 B2764990 B2764990
C 488 16.4 74.5 142 8 BQ975098 BQ975098
C 489 16.4 74.5 149 5 CD738057 CD738057
C 490 16.4 74.5 161 6 CA733208 CA733208
C 491 16.4 74.5 199 6 CD378057 CD378057
C 492 16.4 74.5 261 4 BG906745 BG906745
C 493 16.4 74.5 280 1 AJ769564 AJ769564
C 494 16.4 74.5 291 2 BE404053 BE404053
C 495 16.4 74.5 300 2 BE401214 BE401214
C 496 16.4 74.5 360 1 AU070207 AU070207
C 497 16.4 74.5 362 2 BE122502 BE122502
C 498 16.4 74.5 373 2 BE587223 BE587223
C 499 16.4 74.5 382 2 BE428692 BE428692
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## ALIGNMENTS

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RESULT 1
LOCUS BE938539 315 bp mRNA linear EST 02-OCT-2000
DEFINITION RCO-TN0080-160800-024-a02 TN0080 Homo sapiens CDNA, mRNA sequence.
ACCESSION BE938539
VERSION BE938539.1 GI:10465968
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 315)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jorgensen,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

```

```

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

```

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=822=RC0-TN0080-160  
800-024-a02&3=2000-08-16&t4=1)

Seq primer: puc 18 forward  
High quality sequence start: 27  
High quality sequence stop: 315.  
Location/Qualifiers

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_1lb="TN0080"

/note="Organ: testis normal; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 315;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 TTCCGAGTCTCGATGAGAT 21  
|||||  
221 TTCCGAGTCTCGATGAGAT 241

## Db

RESULT 2  
BM151906/c 383 bp mRNA linear EST 30-NOV-2001  
LOCUS TCBAP1B136 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP136, mRNA  
sequence.

ACCESSION BM151906  
VERSION BM151906.1 GI:17175760  
KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 383)  
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,  
Gunnarathne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.

Pediatric Leukemia cDNA Sequencing Project (2001)  
Unpublished (2001)

CONTACT: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@ccc.org

Seq primer: M13 primer.  
Location/Qualifiers

## FEATURES

source

1..383  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TCBAP136"

/sex="male"  
/issue\_type="leukopheresis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"  
/clone\_1lb="Pediatric pre-B cell acute lymphoblastic  
leukemia Baylor-HGSC project=TCBA"  
/note="Vector: lambda PSB; Site\_1: BamHI; Site\_2: EcoRI;

First strand cDNA was primed with an anchored  
XhoI-oligo(dT) primer [5'-GAGAGCTCGAGCGCGGAGAGAG(T)VN  
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand  
was primed with a BamHI-dC primer  
[5'-AGAGCTCGAGTCCGCGCGCGGATTAATTAAT(C) 3'].

Double-stranded cDNA was then digested with BamHI and XhoI  
and directionally cloned into the BamHI and SalI sites of  
lambda PSB vector. Library was constructed by Wei Yu at RIKEN  
of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T,  
Itoh M., Nagaoka S., Sasaki, Okazaki Y., Muramatsu M,  
Schneider C., Hayashizaki Y., High efficiency selection of  
full-length cDNA by improved biotinylated cap trepper,  
DNA Res 4: 1, 61-6, Feb 28, 1997")

## ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 383;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 TTCCGAGTCTCGATGAGAT 21  
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310 TTCCGAGTCTCGATGAGAT 290

## Db

RESULT 3  
BM193168/c 453 bp mRNA linear EST 13-DEC-2001  
LOCUS TCBAP1E10621 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1062, mRNA  
sequence.

ACCESSION BM193168  
VERSION BM193168.1 GI:17651403  
KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 453)  
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,  
Gunnarathne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.

Pediatric Leukemia cDNA Sequencing Project (2001)  
Unpublished (2001)

CONTACT: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@ccc.org

Seq primer: M13 primer.  
Location/Qualifiers

## FEATURES

source

1..453  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TCBAP1062"

/sex="male"  
/issue\_type="leukopheresis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"  
/clone\_1lb="Pediatric pre-B cell acute lymphoblastic  
leukemia Baylor-HGSC project=TCBA"  
/note="Vector: lambda PSB; Site\_1: BamHI; Site\_2: EcoRI;  
First strand cDNA was primed with an anchored  
XhoI-oligo(dT) primer [5'-GAGAGCTCGAGCGCGGAGAGAG(T)VN  
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand  
was primed with a BamHI-dC primer  
[5'-AGAGCTCGAGTCCGCGCGCGGATTAATTAAT(C) 3'].  
Double-stranded cDNA was then digested with BamHI and XhoI  
and directionally cloned into the BamHI and SalI sites of  
lambda PSB vector. Library went through one round of

## ORIGIN

normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T., Itoh M., Nagaoaka S., Sasaki N., Okazaki Y., Muramatsu M., Schneider C., Hayashizaki Y., High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"

Query Match 95.5%; Score 21; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
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Db 310 TTCCGAGTTCTCGATGAGAT 290

RESULT 4  
AW844829/c 464 bp mRNA linear EST 18-MAY-2000  
LOCUS RC3-CN0056-010400-016-C04 CN0056 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW844829

ACCESSION AW844829.1 GI:7938812

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 464)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Ngai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2=RC3-CN0056-010

400-016-c04&t3=2000-04-01&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 20

High quality sequence stop: 464.

Location/Qualifiers

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/organism="Homo sapiens"

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/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="CN0056"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORSPERS PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 20;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
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Db 50 TTCCGAGTTCTCGATGAGAT 30

RESULT 5  
BE245815/c 474 bp mRNA linear EST 03-OCT-2001  
LOCUS TCBAPIE3171 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAPI3171, mRNA

ACCESSION BE245815

VERSION BE245815.1 GI:9097562

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 474)

Wei, Y., Tsang, Y.T.M., Mei, G., Xu, J.M., Ali-Osman Jr., F.R.,

Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.

Pediatric leukemia cDNA Sequencing Project

Unpublished (2000)

Contact: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center

at Baylor College of Medicine

1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536

Fax: 832-825-4038

Email: clones@txccc.org

Citation: Carninci, P. and Hayashizaki, Y. High efficiency

full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Seq primer: M13 primer.

Location/Qualifiers

1..474

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="TCBAP3171"

/sex="male"

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/cell\_type="pre-B cell"

/dev\_stage="pediatric 2 years"

/lab\_host="DH10B"

/clone\_lib="Pediatric pre-B cell acute lymphoblastic

leukemia Baylor-HGSC project=TCBA"

/note="Vector: lambda pSB; Site 1: BamHI; Site 2: SmaI;

First strand cDNA was primed with an anchored

XhoI-oligo(dT) primer [5'GAGGAGCTCGAGCGCGAGGAG(T)VN

3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand

was primed with a BamHI-dC primer

[5'AGAGAGCTCGATCGCGCGCGCATTAATATAT(C) 3']

Double-stranded cDNA was then digested with BamHI and XhoI

and directionally cloned into the BamHI and SmaI sites of

lambda pSB vector. Library was through one round of

normalization. Library was constructed by Wei Yu at RIKEN

of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T.,

Itoh M., Nagaoaka S., Sasaki N., Okazaki Y., Muramatsu M.,

Schneider C., Hayashizaki Y., High efficiency selection of

full-length cDNA by improved biotinylated cap trapper.,

DNA Res 4: 1, 61-6, Feb 28, 1997)"

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 474;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCTCGATGAGAT 21  
|||||

Db 390 TTCCGAGTTCTCGATGAGAT 370

RESULT 6  
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LOCUS BF841366 475 bp mRNA linear EST 13-JAN-2001  
DEFINITION RC2:HT1079-011200-014-d09 HT1079 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF841366  
VERSION BF841366.1 GI:12194291  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 475)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
JOURNAL  
MEDLINE  
PUBMED  
10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2&t=RC2-HT1079-011200-014-d09&c=2000-12-01&t=1)  
Seq primer: puc 18 forward  
High quality sequence start: 18  
High quality sequence stop: 473.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
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/note="Organ: head neck; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORBSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 475;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGAGTTCTCGATGAGAT 21  
DB 34 TTGGGAGTTCTCGATGAGAT 14

RESULT 7  
BX475238/c

LOCUS BX475238 496 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp686N24175.t1 686 (synonym: hlc3) Homo sapiens cDNA clone  
ACCESSION DKFZp686N24175.5', mRNA sequence.  
VERSION BX475238  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 496)  
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, W. and Wiemann, S.  
EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
Unpublished (2003)  
CONTACT: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine University, Duesseeldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No si sequence available.  
This clone (DKFZp686N24175) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.  
Location/Qualifiers  
1. 496  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686N24175"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlc3)"  
/note="Vector: pTriblax2; Site\_1: SfiIA; Site\_2: SfiIB; cDNA-collection"

FEATURES  
source

ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 496;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGAGTTCTCGATGAGAT 21  
DB 485 TTGGGAGTTCTCGATGAGAT 465

RESULT 8  
BE244425/c

LOCUS BE244425 512 bp mRNA linear EST 03-OCT-2001  
DEFINITION TCBAP2E1627 Pediatric pre-B cell acute lymphoblastic leukemia  
Baylor-HMSC project=TCBA Homo sapiens cDNA clone TCBAP1627, mRNA sequence.  
ACCESSION BE244425  
VERSION BE244425.1 GI:9096166  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 512)  
Wei, Y., Tsang, Y.-T.M., Mei, G., Xu, J.M., Ali-Osman, J.R., Wuzy, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
Pediatric leukemia cDNA Sequencing Project  
Unpublished (2000)  
Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@tccc.org  
Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M13 primer.  
Location/Qualifiers  
1. 512  
/organism="Homo sapiens"

FEATURES  
source

## ORIGIN

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TCBAP1627"  
/sex="male"  
/tissue\_type="leukopheresis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH108"  
/clone\_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"  
/note="Vector: lambda PSB; Site 1: BamHI; Site 2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer (5'-GGAGGACTCGAGCGCCGAGAGAG(T)VN 3'; V=A,C,G; N=A,C,G,T) and then dg tailed. Second strand was primed with a BamHI-dc primer (5'-AGAGCTCGATCCGCGCCGCAATATATAT(C) 3'). Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda PSB vector. Library was constructed by Wei Yu at RIKEN of Japan (Garninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki Y, Hayashizaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper.", DNA Res 4: 1, 61-6, Feb 28, 1997)"

## Query Match

Best Local Similarity 100.0%; Pred. No. 20; Length 512;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGAGTTCTCGATGAGAT 21  
Db 274 TTGCGAGTTCTCGATGAGAT 254

RESULT 9 BE391006 515 bp mRNA linear EST 21-JUN-2000  
LOCUS 60128561F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3607443 5',  
DEFINITION mRNA sequence.

ACCESSION BE391006  
VERSION BE391006.1 GI:93636371  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 515)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LNCM258 Row: 1 Column: 04  
High quality sequence stop: 506.  
Location/Qualifiers

## FEATURES

1. 515  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3607443"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH108 (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"

## ORIGIN

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Qy 1 TTGCGAGTTCTCGATGAGAT 21  
Db 476 TTGCGAGTTCTCGATGAGAT 456

RESULT 10 BE244892 520 bp mRNA linear EST 03-OCT-2001  
LOCUS TCBAP162779 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP2779, mRNA sequence.

ACCESSION BE244892  
VERSION BE244892.1 GI:9096722  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 520)  
AUTHORS Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
TITLES Pediatric Leukemia cDNA Sequencing Project  
JOURNAL Unpublished (2000)  
COMMENT Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@xccc.org  
Citation: Garninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M13 primer.

## FEATURES

1. 520  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="TCBAP2779"  
/sex="male"  
/tissue\_type="leukopheresis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH108"  
/clone\_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"  
/note="Vector: lambda PSB; Site 1: BamHI; Site 2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer (5'-GGAGGACTCGAGCGCCGAGAGAG(T)VN 3'; V=A,C,G; N=A,C,G,T) and then dg tailed. Second strand was primed with a BamHI-dc primer (5'-AGAGCTCGATCCGCGCCGCAATATATAT(C) 3'). Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda PSB vector. Library was constructed by Wei Yu at RIKEN of Japan (Garninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki Y, Hayashizaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper.",



ORIGIN DNA Res 4: 1, 61-6, Feb 28, 1997"

Query Match 95.5%; Score 21; DB 2; Length 520;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCGATGAGAT 21  
|||||  
Db 420 TTGGAGTTCGATGAGAT 400

RESULT 11  
BE243851/c 522 bp mRNA linear EST 03-OCT-2001  
LOCUS TCBAP1627 Pediatric pre-B cell acute lymphoblastic leukemia  
DEFINITION Baylor-HGSC Project-TCBA Homo sapiens cDNA clone TCBAP1627, mRNA  
Sequence.

ACCESSION BE243851 GI:9095590  
VERSION BE243851  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 522)  
Wei, Y., Tang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R.,  
Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.,  
Pediatric Leukemia cDNA Sequencing Project  
Unpublished (2000)  
TITLE Contact: Dr. Judith F. Margolin  
JOURNAL Texas Children's Cancer Center and Human Genome Sequencing Center  
COMMENT at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clone@ccc.org  
Citation: Carninci, P. and Hayashizaki, Y. High efficiency  
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M3 primer

FEATURES  
source location/Qualifiers  
1..522  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="TCBAP1627"  
/sex="male"  
/tissue\_type="Leukoparesis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"  
/clone\_1b="Pediatric pre-B cell acute lymphoblastic  
leukemia Baylor-HGSC Project-TCBA"  
/note="vector: lambda psb; site 1: BamHI; Site 2: EcoRI,  
first strand cDNA was primed with an anchored  
xhoi-oligo(dT) primer [5'-GAGAGCTCGAGCGCGCAGAGCAG(T)VN  
3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand  
was primed with a BamHI-dC primer  
[5'-AGAGAGCTCGAGCGCGCGCGCAATATATATATAT(C) 3'].  
Double-stranded cDNA was then digested with BamHI and XhoI  
and directionally cloned into the BamHI and SalI sites of  
lambda psb vector. Library was constructed by Wei Yu at RIKEN  
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,  
Itoh M, Nagaoaka S, Sasaki, Okazaki Y, Muramatsu M,  
Schneider C, Hayashizaki Y, High efficiency selection of  
full-length cDNA by improved biotinylated cap trapper.,  
DNA Res 4: 1, 61-6, Feb 28, 1997"

ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 522;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCGATGAGAT 21  
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Db 273 TTGGAGTTCGATGAGAT 253

RESULT 12  
CN337098/c 523 bp mRNA linear EST 16-MAY-2004  
LOCUS 17000470616619 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
DEFINITION CN337098  
ACCESSION CN337098.1 GI:47337032  
VERSION EST.  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 523)  
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,  
Lebkowksi, J. and Stanton, L.W.,  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6) 707-716 (2004)  
CONTACT: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 523 Std Error: 0.00.  
location/Qualifiers

FEATURES  
source 1..523  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone\_1b="GRN\_EB"  
/note="Oligo dT primed, full-length enriched cDNA library  
from embryoid body outgrowths derived from h9 cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

ORIGIN

Query Match 95.5%; Score 21; DB 7; Length 523;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTTCGATGAGAT 21  
|||||  
Db 393 TTGGAGTTCGATGAGAT 373

RESULT 13  
BE019655/c 524 bp mRNA linear EST 06-JUN-2000  
LOCUS db27h04.x1 NIH MGC 5 Homo sapiens cDNA clone IMAGE:2964151 3'  
DEFINITION similar to TR:095966 O95966 TM7XN1 PROTEIN PRECURSOR. ;, mRNA  
sequence.  
ACCESSION BE019655 GI:8279736  
VERSION BE019655.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 524)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 DNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: WGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 image.llnl.gov/image/html/resources.shtml

Possible reversed clone: similarity on wrong strand  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 405.

## FEATURES

## source

1.524  
 /organism="Homo sapiens"  
 /mol\_type="rRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2864151"  
 /tissue\_type="carcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: cervix; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; CDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21

Db 182 TTCCGAGTCTCGATGAGAT 162

RESULT 14  
 AM837046/c 527 bp mRNA linear EST 18-MAY-2000  
 LOCUS  
 DEFINITION QV1-LT0037-150200-069-e09 LT0037 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AM837046  
 VERSION AM837046.1 GI:7931020  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 527)  
 Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,  
 Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,F., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

## REFERENCE

## AUTHORS

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800

## COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?el=et2-qv1-LT0037-150  
 200-069-e09&t3=2000-02-15&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 81.  
 Location/Qualifiers

## FEATURES

## source

1.527  
 /organism="Homo sapiens"  
 /mol\_type="rRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone="LT0037"  
 /note="Organ: leiomyos; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI. A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 527;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21

Db 247 TTCCGAGTCTCGATGAGAT 227

## RESULT 15

## LOCUS

## DEFINITION

BE246307 531 bp mRNA linear EST 03-OCT-2001  
 TCBAPE3B1627 pediatric pre-B cell acute lymphoblastic leukemia  
 Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAPE1627, mRNA  
 sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 531)  
 Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R.,  
 Muzny,D., Bouck,U., Gibbs,R.A. and Margolin,J.F.  
 Pediatric Leukemia cDNA Sequencing Project  
 Unpublished (2000)  
 Contact: Dr. Judith F. Margolin  
 Texas Children's Cancer Center and Human Genome Sequencing Center  
 at Baylor College of Medicine  
 1102 Bates, MC3-3320 Houston, TX 77030, USA  
 Tel: 832-824-4536  
 Fax: 832-824-4038  
 Email: clones@ccc.org  
 Citation: Caranci,P. and Hayashizaki,Y. High efficiency  
 full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Seq primer: M13 primer.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

1.531  
 /organism="Homo sapiens"  
 /mol\_type="rRNA"  
 /db\_xref="taxon:9606"  
 /clone="TCBAPE1627"  
 /sex="male"  
 /tissue\_type="leukopheresis"  
 /cell\_type="pre-B cell"  
 /dev\_stage="pediatric 2 years"  
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 /clone\_lib="pediatric pre-B cell acute lymphoblastic  
 leukemia Baylor-HGSC project=TCBA"  
 /note="Vector: lambda PSB, Site 1: BamHI; Site 2: EcoRI;  
 First strand cDNA was primed with an anchored  
 XhoI-oligo(dT) primer [5'GGAGACTGACGGCCGACGAGAGAG(7)VN

3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dc primer [5'AGAGAGCTCGATCCGCGCCGCAATTAATAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 531;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGTTCGATGAGAT 21  
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Db 274 TTCCGAGTTCGATGAGAT 254

RESULT 16  
BX475095/c 532 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZP686J10174.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZP686J10174 5', mRNA sequence.  
ACCESSION BX475095  
VERSION BX475095.1 GI:31669290  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobbo, G., Han, M., and Wiemann, S.  
EST (Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., et al.)  
Unpublished (2003)  
CONTACT: MIPS

TITLE  
JOURNAL  
COMMENT  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No 5' sequence available.  
This clone (DKFZP686J10174) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

source

1..532  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZP686J10174"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_id="686 (synonym: hlcc3)"  
/note="Vector: pTIPLEX2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 532;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGTTCGATGAGAT 21  
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Db 486 TTCCGAGTTCGATGAGAT 466

RESULT 17  
BX479505/c 535 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZP686H07211.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZP686H07211 5', mRNA sequence.  
ACCESSION BX479505  
VERSION BX479505.1 GI:31915331  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 535)  
Koehler, K., Beyer, A., Mewes, H.W., Well, B., Amid, C., Osanger, A.,  
Fobbo, G., Han, M., and Wiemann, S.  
EST (Koehler, K., Beyer, A., Mewes, H.W., Well, B., Amid, C., et al.)  
Unpublished (2003)  
CONTACT: MIPS

TITLE  
JOURNAL  
COMMENT  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by BMRZ (Biomedical Research Center at the Heinrich-  
Heine-University, Duesseldorf/Germany) within the cDNA sequencing  
consortium of the German Genome Project. No 5' sequence available.  
This clone (DKFZP686H07211) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

source

1..535  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="DKFZP686H07211"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_id="686 (synonym: hlcc3)"  
/note="Vector: pTIPLEX2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 535;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGTTCGATGAGAT 21  
|||||  
Db 432 TTCCGAGTTCGATGAGAT 412

RESULT 18  
BX475102/c 542 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZP686J20174.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZP686J20174 5', mRNA sequence.  
ACCESSION BX475102  
VERSION BX475102.1 GI:31669297  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 542)  
Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., Osanger, A.,  
Fobbo, G., Han, M., and Wiemann, S.  
EST (Bloembergen, H., Boecker, M., Mewes, H.W., Well, B., Amid, C., et al.)  
Unpublished (2003)  
CONTACT: MIPS

TITLE  
JOURNAL  
COMMENT  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,  
 sequenced by GAP (National Research Centre for Biotechnology Ltd.,  
 Braunschweig/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No 3' sequence available.  
 This clone (DKFZ66320174) is available at the RZPD in Berlin.  
 Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

## source

1..542  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZ66320174"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_idb="686 (synonym: h1cc3)"  
 /note="Vector: pTriplex2; Site\_1: sf1A; Site\_2: sf1B;  
 cDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 TTGGAGTTCTCGATGGAGAT 21  
 |||||  
 500 TTGGAGTTCTCGATGGAGAT 480

## Db

RESULT 19  
 CA390929/c 559 bp mRNA linear EST 06-NOV-2002  
 LOCUS c116c02.y1 Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone c116c02  
 5', mRNA sequence.

ACCESSION CA390929  
 VERSION CA390929.1 GI:24722374  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 559)

TITLE Wistow, G., Bernstein, S.L., Wyatt, M.K., Parris, R.N., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
 Expressed sequence tag analysis of human RPE/choroid for the  
 NIHBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants

JOURNAL M.O.L. Vols. 8 (4), 205-220 (2002)  
 MEDLINE 22103460  
 PUBMED 12107410

## COMMENT

Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: g.wistow@nih.gov  
 Plate: 116 row: c column: 02  
 Seq primer: M13RPI reverse primer (ABI).  
 Location/Qualifiers

## FEATURES

## source

1..559  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="c116c02"  
 /tissue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_idb="Human Retinal pigment epithelium/choroid cDNA"

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 559;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 TTGGAGTTCTCGATGGAGAT 21  
 |||||  
 435 TTGGAGTTCTCGATGGAGAT 415

## Db

RESULT 20  
 BE206268/c 568 bp mRNA linear EST 18-SEP-2000  
 LOCUS b966e12.x1 NIH MGC 5 Homo sapiens cDNA clone IMAGE:2925166 3'  
 DEFINITION similar to TR:095966 O95966 TM7XN1 PROTEIN PRECURSOR. ; mRNA  
 sequence.

ACCESSION BE206268  
 VERSION BE206268.1 GI:8749666  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 568)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 image.lnl.gov/image/html/lresources.shtml

Possible reversed clone: similarity on wrong strand  
 Seg primer: -40UP from Gibco  
 High quality sequence stop: 477.  
 Location/Qualifiers

## FEATURES

## source

1..568  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2925166"  
 /tissue\_type="carcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_idb="NIH\_MGC\_5"  
 /note="Organ: cervix; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACAGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

	Query Match Similarity	95.5%;	Score 21;	DB 2;	Length 568;
	Best Local Similarity	100.0%;	Pred. No. 21;		
	Matches 21; Conservative	0;	Mismatches	0;	Gaps 0;
Oy	1 TTCGAGTTCGTGATGAGAT 21				
Db	298 TTCGAGTTCGTGATGAGAT 278				
RESULT 21	AL707342	570 bp	mRNA	linear	EST 04-SEP-2003
LOCUS	DKFZP666C1647.r1.686 (synonym: hicc3)	Homo sapiens cDNA clone			
DEFINITION	DKFZP666C1647.5', mRNA sequence.				
ACCESSION	AL707342				
VERSION	AL707342.1	GI:19690697			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (baes 1 to 570) Otenwelder,B., Obermaier,B., Mewes,W., Mewes,H.W., weil,B. and Wieman,S. EST (Otenwelder,B., Obermaier,B., Mewes,H.W., weil,B. and Wieman,S.) Unpublished (2001)				
REFERENCE	Contact: MIPS				
AUTHORS	MIPS				
TITLE	Ingsletteder Landstr.1, D-85764 Neuberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German genome project. No si sequence available. This clone (DKFZP666C1647) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.				
JOURNAL	Location/Qualifiers				
COMMENT	1..570 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DKFZP666C1647" /dev_stage="adult" /lab_host="DH10B" /clone_1ib="686 (synonym: hicc3)" /note="Vector: pTriplex2; Site_1: sfIRA; Site_2: sfIRB; cDNA-collection"				
FEATURES	ORIGIN				
SOURCE	Query Match 95.5%; Score 21; DB 1; Length 570; Best Local Similarity 100.0%; Pred. No. 21; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1 TTCGAGTTCGTGATGAGAT 21				
Db	537 TTCGAGTTCGTGATGAGAT 517				
RESULT 22	AL598371	573 bp	mRNA	linear	EST 04-SEP-2003
LOCUS	DKFZP313A0720.r1.313 (synonym: hlccl)	Homo sapiens cDNA clone			
DEFINITION	DKFZP313A0720.5', mRNA sequence.				
ACCESSION	AL598371				
VERSION	AL598371.1	GI:15161062			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

```

REFERENCE      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS       1 (bases 1 to 573)
               Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
               Wiemann,S.
TITLE         EST (duesterhoeft, et al.)
JOURNAL       Unpublished (1999)
COMMENT       Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
this is the 5' sequence of the clone insert
This clone (DKFPz686K09174_r1) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES
source
1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFPz686K09174"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1db="313 (synonym: hlcc2)"
/ncseq=vector: pTribEx2; site_1: sf1A; site_2: sf1B;
cdna-collection"

ORIGIN
Query Match 95.5%; Score 21; DB 1; Length 573;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTGGAGGTTCCGATGGAGAT 21
|||||
513 TTGGAGGTTCCGATGGAGAT 493

RESULT 23 583 bp mRNA linear EST 04-SEP-2003
BX475118/c
LOCUS
DEFINITION DKFPz686K09174_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone
DKFPz686K09174_5', mRNA sequence.
ACCESSION BX475118
VERSION BX475118
KEYWORDS BX475118.1 GI:31669313
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Bloecker,H., Boecker,M., Mewes,H.W., Weill,B., Amid,C., Oeanger,A.,
Pobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Boecker,M., Mewes,H.W., Weill,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
This clone (DKFPz686K09174) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES
source
1..583
/organism="Homo sapiens"

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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686K09174"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_idb="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; site\_1: sf1A; site\_2: sf1B;  
CDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 583;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
|||||  
DB 455 TTCCGAGTCTCGATGAGAT 435

## RESULT 24

BX506361/c 601 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp686N14249.r1.686 (synonym: hlcc3) Homo sapiens CDNA clone  
DEFINITION DKFZp686N14249.5', mRNA sequence.  
ACCESSION BX506361  
VERSION BX506361.1 GI:32040060  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 601)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Mewes, H.W., Well, B., Amd, C., Osanger, A., Fobo, G., Han, M., and  
Wiemann, S., Krieger, S., Regier, T., Rittmüller, C., et al.)  
EST (Ansoerge, W., Krieger, S., Regier, T., Rittmüller, C., et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp686N14249) is available at the RZPD in Berlin.  
Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

1..601  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686N14249"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_idb="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; site\_1: sf1A; site\_2: sf1B;  
CDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 601;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
|||||  
DB 384 TTCCGAGTCTCGATGAGAT 364

## RESULT 25

BX485768/c 607 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp686I13248.r1.686 (synonym: hlcc3) Homo sapiens CDNA clone  
DEFINITION DKFZp686I13248.5', mRNA sequence.  
ACCESSION BX485768  
VERSION BX485768.1 GI:31948835  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 607)  
Ottewaelde, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,  
Well, B., Amd, C., Osanger, A., Fobo, G., Han, M., and Wiemann, S.  
EST (Ottewaelde, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,  
et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the German Genome Project. No sl sequence  
available.  
This clone (DKFZp686I13248) is available at the RZPD in Berlin.  
Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

1..607  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686I13248"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_idb="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; site\_1: sf1A; site\_2: sf1B;  
CDNA-collection"

## ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 607;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
|||||  
DB 400 TTCCGAGTCTCGATGAGAT 380

RESULT 26  
BG819058/c 613 bp mRNA linear EST 22-MAY-2001  
LOCUS BG819058.1 NC1 CGAP\_Brn67 Homo sapiens CDNA clone IMAGE:4932318  
DEFINITION 5', mRNA sequence.  
ACCESSION BG819058  
VERSION BG819058.1 GI:14166645  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 613)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Query Match 95.5%; Score 21; DB 5; Length 613;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
|||||  
DB 400 TTCCGAGTCTCGATGAGAT 380



Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Plate: LLM10857 row: 0 column: 07  
High quality sequence stop: 612.  
Location/Qualifiers

## FEATURES

1. 613

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4932318"

/issue\_type="anaplastic oligodendroglioma with 1p/19q loss"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_1ib="NCI CGAP Brn67"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: Sali; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

## ORIGIN

## Query Match

95.5%; Score 21; DB 4; Length 613;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGAGTTCTCGATGAGAT 21

DB 255 TTGGAGTTCTCGATGAGAT 235

RESULT 27  
BG819937 618 bp mRNA linear EST 22-MAY-2001  
LOCUS 602782040F1 NCI CGAP Brn67 Homo sapiens CDNA clone IMAGE:4933089  
DEFINITION 5', mRNA sequence.

ACCESSION BG819937 GI:14167524

VERSION BG819937.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 618)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM10859 row: 0 column: 10

High quality sequence stop: 616.

Location/Qualifiers

1. 618

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4933089"

/issue\_type="anaplastic oligodendroglioma with 1p/19q loss"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_1ib="NCI CGAP Brn67"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: Sali; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

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Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Technology. Note: this is a NCI CGAP Library."

Query Match 95.5%; Score 21; DB 4; Length 618;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGAGTTCTCGATGAGAT 21

DB 521 TTGGAGTTCTCGATGAGAT 501

## FEATURES

1. 636

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5203583"

/lab\_host="DH10B"

/clone\_1ib="NIH-MGC 122"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: EcorV (destroyed); RNA source

anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt

primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note: this is a NIH-MGC Library."

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM1510 row: e column: 24

High quality sequence stop: 632.

Location/Qualifiers

1. 636

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5203583"

/lab\_host="DH10B"

/clone\_1ib="NIH-MGC 122"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: EcorV (destroyed); RNA source

anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt

primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note: this is a NIH-MGC Library."

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM1510 row: e column: 24

High quality sequence stop: 632.

Location/Qualifiers

1. 636

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5203583"

/lab\_host="DH10B"

/clone\_1ib="NIH-MGC 122"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: EcorV (destroyed); RNA source

anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt

primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note: this is a NIH-MGC Library."

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM1510 row: e column: 24

High quality sequence stop: 632.

Location/Qualifiers

1. 636

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5203583"

/lab\_host="DH10B"

/clone\_1ib="NIH-MGC 122"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: EcorV (destroyed); RNA source

anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt

primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note: this is a NIH-MGC Library."

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM1510 row: e column: 24

High quality sequence stop: 632.

Location/Qualifiers

1. 636

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5203583"

/lab\_host="DH10B"

/clone\_1ib="NIH-MGC 122"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site\_1: NCI; Site\_2: EcorV (destroyed); RNA source

anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dt

primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 643)  
Kale, P. I., Harsch, T. J., Folta, P. A., Nelson, D. O., Sanders, C. G. and Prange, C. K.

AUTHORS The I.M.A.G.E. Consortium quality control effort: clone

TITLE resequencing for verification

JOURNAL Unpublished (2001)

COMMENT Contact: Prange CK  
The I.M.A.G.E. Consortium  
Lawrence Livermore National Laboratory  
Livermore, CA, USA  
Email: help@image.llnl.gov  
This read has been produced as part of the I.M.A.G.E. of the sequence. For information on obtaining this clone, please contact info@image.llnl.gov.  
plate: LLAM9485 row: n column: 3  
Seq primer: ml3rpl  
High quality sequence stop: 643.

FEATURES  
Source  
1..643  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4178114"  
/issue\_type="anaplastic oligodendroglioma with 1p/19q loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI\_CGAP Brn67"  
/note="Organ: Brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 643;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGGAGAT 21  
|||||

Db 522 TTGGAGTTCTCGATGGAGAT 502  
|||||

RESULT 30  
AL046540/c 649 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp34G178\_r1 434 (synonym: htes3) Homo sapiens cDNA clone  
DEFINITION DKFZp34G178 5', mRNA sequence.  
ACCESSION AL046540  
VERSION AL046540.1 GI:5434608  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 649)  
Ottensmeyer, B., Obermaier, B., Mewes, H. W., Gassenhuber, J. and Wiemann, S.  
EST (Ottensmeyer, et al.)  
Unpublished (1999)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de  
Sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No 5' sequence available.  
This clone (DKFZp34G178) is available at the RZPD in Berlin.

FEATURES  
Source  
1..649  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4828710"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC 97"  
/note="Organ: testis; Vector: pBluescriptPR (modified pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gicgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTT-3', size-selected for average insert size 2.2 kb and normalized for R0T 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library..."

ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 682;

RESULT 31  
BG718773/c 682 bp mRNA linear EST 08-MAY-2001  
LOCUS 602696925F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4828710 5',  
DEFINITION mRNA sequence.  
ACCESSION BG718773  
VERSION BG718773.1 GI:13997960  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 682)  
NIH-MGC <http://mgc.nhl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Straube, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
plate: LLAM10747 row: b column: 07  
High quality sequence stop: 283.

FEATURES  
Source  
1..682  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4828710"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC 97"  
/note="Organ: testis; Vector: pBluescriptPR (modified pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gicgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTT-3', size-selected for average insert size 2.2 kb and normalized for R0T 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library..."

ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 682;

please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: [clone@rzpd.de](mailto:clone@rzpd.de).  
Location/Qualifiers  
1..649  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp34G178"  
/issue\_type="testis"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="434 (synonym: htes3)"  
/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTCTCGATGAGAT 21  
|||||  
586 TTGGAGTCTCGATGAGAT 566

RESULT 32  
B1666902/c 697 bp mRNA linear EST 12-SEP-2001  
LOCUS 603291647F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:511282 5',  
DEFINITION mRNA sequence.  
ACCESSION B1666902  
VERSION B1666902.1 GI:15581135  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 697)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Place: L1AM11788 row: m column: 11  
High quality sequence stop: 674.  
Location/Qualifiers  
1. 697

FEATURES  
Source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:511282"  
/issue\_type="hypothalamus"  
/lab\_host="DH10B"  
/clone\_1ib="NIH\_MGC\_96"  
/note="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
(gtcgag); Oligo-dT primed using primer  
5'-TTTTTTTTTTTNN-3', size selected for average  
insert size 2.3 kb and normalized to R07 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NHGRI/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC library."

# ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 697;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTCTCGATGAGAT 21  
|||||  
367 TTGGAGTCTCGATGAGAT 347

RESULT 33  
AL133937/c 728 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp761P0614\_F1 761 (synonym: hamy2) Homo sapiens cDNA clone  
DEFINITION DKFZp761P0614 5', mRNA sequence.  
ACCESSION AL133937  
VERSION AL133937.1 GI:6602124

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 728)  
Ansoerge, W., Wilkner, U., Mewes, W., Well, B. and Wiemann, S.  
EST (Ansoerge, W., Wilkner, U., Mewes, W., Well, B. and Wiemann, S.)  
Unpublished (1999)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email: [s.wiemann@dkfz-heidelberg.de](mailto:s.wiemann@dkfz-heidelberg.de);  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.  
No al sequence available.  
This clone (DKFZp761P0614) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: [clone@rzpd.de](mailto:clone@rzpd.de).  
Location/Qualifiers  
1. 728

FEATURES  
Source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp761P0614"  
/issue\_type="amygdala"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_1ib="761 (synonym: hamy2)"  
/note="Vector: pSport1; Site 1: NotI; Site 2: SalI"

# ORIGIN

Query Match 95.5%; Score 21; DB 1; Length 728;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTCTCGATGAGAT 21  
|||||  
393 TTGGAGTCTCGATGAGAT 373

RESULT 34  
B1767127/c 732 bp mRNA linear EST 25-SEP-2001  
LOCUS 603054191F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5203607 5',  
DEFINITION mRNA sequence.  
ACCESSION B1767127  
VERSION B1767127.1 GI:15758705  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 732)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Place: L1AM1510 row: f column: 24  
High quality sequence stop: 724.  
Location/Qualifiers  
1. 732

FEATURES  
Source

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5203607"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleen. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

```

## ORIGIN

```

Query Match      95.5%; Score 21; DB 4; Length 732;
Best Local Similarity 100.0%; Pred.No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  TTCCGAGTCTCGATGAGAT 21
         |||||||
Db      324 TTCCGAGTCTCGATGAGAT 304

```

```

RESULT 35
BI646202/c      741 bp      mRNA      linear      EST 21-AUG-2001
603203030F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:526924 5',
LOCUS DEFINITION mRNA sequence.

```

```

ACCESSION      BI646202
VERSION        BI646202.1 GI:15254858
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      1 (bases 1 to 741)
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: Miklos Palkovics, M.D., Ph.D.
              CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
              Toshiyuki and Piero Carninci (RIKEN)
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

```

```

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM1679 row: e column: 01
High quality sequence stop: 658.
Location/Qualifiers
1..741
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5269224"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTAA-3', size-selected for average
insert size 2.2 kb and normalized to R0.5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, In
preparation). Library constructed by M. Brownstein
(NHGH/NHGR1, National Institutes of Health). Note: this is
a NIH_MGC Library."

```

## FEATURES

source

## ORIGIN

```

Query Match      95.5%; Score 21; DB 4; Length 741;
Best Local Similarity 100.0%; Pred.No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  TTCCGAGTCTCGATGAGAT 21
         |||||||
Db      515 TTCCGAGTCTCGATGAGAT 495

```

```

RESULT 36
BG910316/c      752 bp      mRNA      linear      EST 05-JUN-2001
602805910F1 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4938170
LOCUS DEFINITION 5', mRNA sequence.

```

```

ACCESSION      BG910316
VERSION        BG910316.1 GI:14290792
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      1 (bases 1 to 752)
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: David N. Louis, M.D.
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

```

```

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LHAM0873 row: c column: 03
High quality sequence stop: 548.
Location/Qualifiers
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4938170"
/clone_lib="anaplastic oligodendroglioma with 1p19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

```

## FEATURES

source

## ORIGIN

```

Query Match      95.5%; Score 21; DB 4; Length 752;
Best Local Similarity 100.0%; Pred.No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  TTCCGAGTCTCGATGAGAT 21
         |||||||
Db      302 TTCCGAGTCTCGATGAGAT 282

```

```

RESULT 37
CN337099/c      755 bp      mRNA      linear      EST 16-MAY-2004
17000531597678 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
LOCUS DEFINITION CN337099
ACCESSION      CN337099
VERSION        CN337099.1 GI:47337033
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

## FEATURES

```

source

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 755)  
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 755 Std Error: 0.00.  
Location/Qualifiers  
1..755  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone\_1ib="GRN\_EB"  
/note="Oligo dt primed, full-length enriched cDNA library  
from embryoid body outgrowth derived from hES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

ORIGIN

Query Match 95.5%; Score 21; DB 7; Length 755;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21  
|||||  
516 TTCGAGTTCGATGAGAT 496

RESULT 38  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BG705518 757 bp mRNA linear EST 07-MAY-2001  
602686543F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4818826 5',  
mRNA sequence.  
BG705518  
BG705518.1 GI:13979935  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 757)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki  
Toshiyuki and Piero Carninci (RIKEN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM10721 row: f column: 11  
High quality sequence start: 67  
High quality sequence stop: 469.  
Location/Qualifiers  
1..757  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

FEATURES  
source

ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 757;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGAGTTCGATGAGAT 21  
|||||  
445 TTCGAGTTCGATGAGAT 425

RESULT 39  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BG536985 761 bp mRNA linear EST 03-APR-2001  
60265045F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4689874 5',  
mRNA sequence.  
BG536985  
BG536985.1 GI:13528531  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 761)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM1506 row: i column: 11  
High quality sequence stop: 487.  
Location/Qualifiers  
1..761  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4689874"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1ib="NIH\_MGC\_77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1:  
5'-ATTCTAGAGCCGAGCGCGCGACATC-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.9  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

FEATURES  
source

Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGAT 21  
Db 416 TTCGAGTTCTCGATGAGAT 396

RESULT 40  
LOCUS B1907794/c 773 bp mRNA linear EST 16-OCT-2001  
DEFINITION B03066045F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5215187 5',  
mRNA sequence.  
ACCESSION B1907794  
VERSION B1907794.1 GI:16170642  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incey Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
plate: L1AM1540 row: 1 column: 12  
High quality sequence stop: 773.  
Location/Qualifiers  
1..773

FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5215187"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/note="Vector: PCMV-SPORT6, Site 1: NotI, Site 2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC library."

## ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 773;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGAT 21  
Db 281 TTCGAGTTCTCGATGAGAT 261

RESULT 41  
LOCUS CF995022/c 774 bp mRNA linear EST 25-NOV-2003  
DEFINITION AGENCOURT 15621840 NIH\_MGC\_147 Homo sapiens cDNA clone  
IMAGE:30528961 5', mRNA sequence.  
ACCESSION CF995022  
VERSION CF995022.1 GI:38511082  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 774)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Stefan Haneson  
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.jnl.gov  
plate: NDAM615 row: m column: 02  
High quality sequence stop: 525.  
Location/Qualifiers  
1..774

FEATURES  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30528961"  
/tissue\_type="Human Placenta"  
/lab\_host="DH10B Tona"  
/clone\_1lb="NIH\_MGC\_147"  
/note="Organ Placenta; Vector: pBluescriptR; Site 1:  
all-XhoI; Site 2: BamH; Oligo-dT primed using primer  
5'-TTTTTCTTTTCTTTTCTTTT-3', size-selected for average  
insert size 2.3 kb and normalized to R07 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NHGRI/NHGRI, National Institutes of Health). Note: This is  
a NIH\_MGC library."

## ORIGIN

Query Match 95.5%; Score 21; DB 7; Length 774;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGAT 21  
Db 465 TTCGAGTTCTCGATGAGAT 445

RESULT 42  
LOCUS BQ433220/c 777 bp mRNA linear EST 24-MAY-2002  
DEFINITION AGENCOURT 7723723 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6050606  
5', mRNA sequence.

ACCESSION BQ433220  
VERSION BQ433220.1 GI:21172296  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTB/DTF  
CDNA Library Preparation: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation



Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM13303 row: b column: 15

High quality sequence stop: 436.  
Location/Qualifiers

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1..777
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5264957"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: PCWV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."
```

# ORIGIN

Query Match 95.5%; Score 21; DB 5; Length 777;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
DB 465 TTGGAGTTCTCGATGAGAT 445

RESULT 43  
BI553947 785 bp mRNA linear EST 05-SEP-2001  
LOCUS 603193818P1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5264957 5',  
DEFINITION mRNA sequence.  
VERSION BI553947  
KEYWORDS EST.  
GI:15441259

ACCESSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 785)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strauberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihai  
Toshiyuki and Piero Carninci (RIKEN)  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11668 row: c column: 06  
High quality sequence stop: 688.  
Location/Qualifiers

FEATURES  
source  
1..785  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="5264957"  
/issue\_type="hippocampus"  
/lab\_host="DH10B"  
/clone\_lib="NIH MGC 95"  
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, In

preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC library."

Query Match 95.5%; Score 21; DB 4; Length 785;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
DB 534 TTGGAGTTCTCGATGAGAT 514

RESULT 44  
BI601981 806 bp mRNA linear EST 07-SEP-2001  
LOCUS 603243977P1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5286258 5',  
DEFINITION mRNA sequence.  
VERSION BI601981  
KEYWORDS EST.  
GI:15494920

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 806)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strauberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihai  
Toshiyuki and Piero Carninci (RIKEN)  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11723 row: j column: 19  
High quality sequence stop: 720.  
Location/Qualifiers

FEATURES  
source  
1..806  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_image="5286258"  
/issue\_type="hypothalamus"  
/lab\_host="DH10B"  
/clone\_lib="NIH MGC 96"  
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, In

preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC library."

# ORIGIN

Query Match 95.5%; Score 21; DB 4; Length 806;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGAT 21  
|||||  
DB 530 TTGGAGTTCTCGATGAGAT 510.

RESULT 45

CF995140/c 811 bp mRNA linear EST 25-NOV-2003  
LOCUS  
DEFINITION AGENCOURT\_15621962 NIH\_MGC\_147 Homo sapiens cDNA clone  
IMAGE:30527833 5', mRNA sequence.  
ACCESSION CF995140  
VERSION CF995140.1 GI:38511200  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 811)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm.0A07 Bethesda, MD 20892  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Dr. Stefan Hansson  
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: NDAM612 row: n column: 02  
High quality sequence stop: 640.  
Location/Qualifiers  
1. 811  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30527833"  
/tissue\_type="Human Placenta"  
/lab\_host="DH10B TONa"  
/clone\_1lb="NIH\_MGC\_147"  
/note="Organ: placenta; Vector: pBluescript; Site: 1:  
all-XhoI; Site 2: BamH; Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTNN-3', size-selected for average  
insert size 2.3 kb and normalized to R07 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: This is  
a NIH\_MGC library."

ORIGIN  
Query Match 95.5%; Score 21; DB 7; Length 811;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGAGTCTCGATGGAGAT 21  
|||||  
Db 525 TTCCGAGTCTCGATGGAGAT 505

RESULT 46  
CD246163 817 bp mRNA linear EST 22-MAY-2003  
LOCUS  
DEFINITION AGENCOURT\_14127031 NIH\_MGC\_145 Homo sapiens cDNA clone  
IMAGE:6912793 5', mRNA sequence.  
ACCESSION CD246163  
VERSION CD246163.1 GI:31006627  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 817)  
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: IRB101 row: d column: 12  
High quality sequence stop: 692.  
Location/Qualifiers  
1. 817  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6912793"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_1lb="NIH\_MGC\_145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XbaI/XhoI-3',  
5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1-presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1-presv.dat)  
a Note: this is a NIH\_MGC library."

ORIGIN  
Query Match 95.5%; Score 21; DB 6; Length 817;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGAGTCTCGATGGAGAT 21  
|||||  
Db 202 TTCCGAGTCTCGATGGAGAT 182

RESULT 47  
CB987979 827 bp mRNA linear EST 01-MAY-2003  
LOCUS  
DEFINITION AGENCOURT\_13902574 NIH\_MGC\_147 Homo sapiens cDNA clone  
IMAGE:30340483 5', mRNA sequence.  
ACCESSION CB987979  
VERSION CB987979.1 GI:30282499  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 827)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Dr. Stefan Hansson  
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: NDAM370 row: g column: 20  
High quality sequence stop: 491.  
Location/Qualifiers  
1. 827  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30340483"  
/cissue\_type="Human Placenta"  
/lab\_host="DH10B Tora"  
/clone\_1ib="NIH\_MGC\_147"  
/note="Organ: Placenta; Vector: pBluescriptR, Site\_1:  
all-XhoI; Site\_2: BamHI; Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to R0T 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Garnick, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: This is  
a NIH\_MGC library."

## ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 827;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGTTCGATGAGAT 21  
Db 525 TTGGAGTTCGATGAGAT 505

RESULT 48  
BP125765/c 835 bp mRNA linear EST 24-OCT-2000  
DEFINITION 601763157/1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4025774 5',  
mRNA sequence.  
ACCESSION BP125765  
VERSION BP125765.1 GI:10964805  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 835)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC/DC/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L16M855 row: b column: 15  
High quality sequence stop: 646.  
Location/Qualifiers

## FEATURES

SOURCE

1..835  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4025774"  
/cissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1ib="NIH\_MGC\_20"  
/note="Organ: skin; Vector: pOT57; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 835;  
Best Local Similarity 100.0%; Pred. No. 22;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGAGTTCGATGAGAT 21  
Db 470 TTGGAGTTCGATGAGAT 450

RESULT 49  
AL598478/c 840 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp313J2220 r1 313 (synonym: h1cc2) Homo sapiens cDNA clone  
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ACCESSION AL598478  
VERSION AL598478.1 GI:15161169  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 840)  
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.  
EST (Duesterhoeft, et al.)  
Unpublished (1999)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by Oigen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No 5' sequence available.  
This clone (DKFZp313J2220) is available at the RZPD in Berlin.  
Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

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## ORIGIN

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OY 1 TTGGAGTTCGATGAGAT 21  
Db 366 TTGGAGTTCGATGAGAT 346

RESULT 50  
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VERSION BE893273.1 GI:10354467  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 854)  
NIH-MGC http://mgi.nci.nih.gov/.  
Mammalian Gene Collection (MGC)  
National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL COMMENT

Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DMP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
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 Location/Qualifiers

## FEATURES

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## ORIGIN

Query Match 95.5%; Score 21; DB 2; Length 854;  
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 Db 403 TTCCGAGTTCTCGATGAGAT 383

Search completed: February 2, 2005, 01:27:37  
 Job time : 3028 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: February 1, 2005, 23:58:58 ; Search time 84 Seconds  
(without alignments)  
186.159 Million cell updates/sec

Title: US-10-073-054-14  
Perfect score: 22  
Sequence: 1 ttcgagcttcgcagagagatc 22

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 4	16.4	74.5	3267	4	US-09-252-991A-10707 Sequence 10707, A
C 5	16.2	73.6	519	4	US-09-252-991A-14488 Sequence 14488, A
C 6	16.2	73.6	1347	4	US-09-252-991A-15133 Sequence 15133, A
C 7	16.2	73.6	1465	4	US-09-252-991A-14625 Sequence 14625, A
C 8	16.2	73.6	1446	4	US-09-252-991A-15137 Sequence 15137, A
C 9	16.2	73.6	2001	4	US-09-689-012-1 Sequence 1, Appli
C 10	16.2	73.6	2010	3	US-09-240-410-1 Sequence 1, Appli
C 11	16.2	73.6	2154	4	US-09-252-991A-14624 Sequence 14624, A
C 12	16.2	73.6	2498	3	US-09-041-236-1 Sequence 1, Appli
C 13	16.2	73.6	2622	4	US-09-771-467C-1 Sequence 15001, A
C 14	16.2	73.6	2692	4	US-09-252-991A-15001 Sequence 15001, A
C 15	15.8	71.8	550	4	US-09-668-751-133 Sequence 133, App
C 16	15.8	71.8	744	4	US-09-270-767-14247 Sequence 14247, A
C 17	15.8	71.8	636	4	US-09-248-796A-414 Sequence 414, App
C 18	15.8	71.8	1586	4	US-09-270-767-11307 Sequence 11307, A
C 19	15.8	71.8	1836	4	US-09-252-991A-6042 Sequence 6042, App
C 20	15.8	71.8	1911	4	US-09-252-991A-6258 Sequence 6258, App
C 21	15.6	70.9	251	4	US-09-016-434-320 Sequence 320, App
C 22	15.6	70.9	393	4	US-09-328-352-3744 Sequence 3744, App
C 23	15.6	70.9	1095	4	US-09-602-787A-199 Sequence 199, App
C 24	15.6	70.9	1371	4	US-09-492-709A-196 Sequence 196, App
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C 27	15.6	70.9	36470	4	US-08-311-731A-123 Sequence 123, App

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C 30	15.4	70.0	1686	4	US-09-799-451-327 Sequence 327, App
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C 67	14.8	67.3	972	4	US-09-270-767-10210 Sequence 4887, App
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C 75	14.8	67.3	2437	2	US-09-489-039A-5215 Sequence 3310, App
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C 82	14.8	67.3	45175	4	US-09-453-702B-116 Sequence 117, App
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C 84	14.8	66.4	50	1	US-08-687-443-117 Sequence 1812, App
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C 86	14.6	66.4	50	3	US-09-313-234A-1812 Sequence 13071, A
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C 91	14.6	66.4	423	1	US-08-470-179-71 Sequence 447, App
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C 95	14.6	66.4	532	3	US-09-252-991A-4405 Sequence 143, App
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C 97	14.6	66.4	584	3	US-08-998-416-133 Sequence 954, App
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C 99	14.6	66.4	638	3	US-08-998-416-133 Sequence 954, App
C 100	14.6	66.4	641	4	US-09-620-312D-954 Sequence 954, App

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C 102	14.6	66.4	636	4	US-09-149-476-92	Sequence 92, Appl	C 175	14.6	66.4	3198	4	US-09-252-991A-15066	Sequence 15066, A
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C 104	14.6	66.4	729	4	US-09-270-767-2325	Sequence 2325, A	C 177	14.6	66.4	3435	4	US-09-252-991A-10017	Sequence 10017, A
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C 106	14.6	66.4	834	4	US-09-248-796A-1248	Sequence 1248, Ap	C 179	14.6	66.4	3435	4	US-09-710-279-4114	Sequence 4114, Ap
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C 108	14.6	66.4	852	4	US-09-270-767-844	Sequence 844, App	C 181	14.6	66.4	3842	5	PCT-US93-03076-1	Sequence 1, Appl
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C 120	14.6	66.4	1061	4	US-09-270-767-14581	Sequence 14581, A	C 193	14.6	66.4	1230025	4	US-09-198-452A-1	Sequence 1, Appl
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C 123	14.6	66.4	1128	3	US-09-551-322-1	Sequence 1, Appl	C 196	14.6	66.4	4411529	3	US-09-103-840A-2	Sequence 1, Appl
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C 126	14.6	66.4	1271	4	US-09-737-626A-10	Sequence 310, App	C 199	14.4	65.5	281	4	US-09-270-767-15688	Sequence 15688, A
C 127	14.6	66.4	1282	4	US-09-221-017B-310	Sequence 10, Appl	C 200	14.4	65.5	460	2	US-08-487-727A-1	Sequence 1, Appl
C 128	14.6	66.4	1287	4	US-09-914-81A-2	Sequence 2, Appl	C 201	14.4	65.5	514	4	US-09-270-767-7481	Sequence 7481, Ap
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C 131	14.6	66.4	1404	4	US-09-469-039A-5117	Sequence 5137, Ap	C 204	14.4	65.5	2733	4	US-09-602-787A-577	Sequence 577, App
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C 133	14.6	66.4	1443	4	US-09-252-991A-6853	Sequence 6853, Ap	C 206	14.4	65.5	3812	1	US-08-188-882-19	Sequence 19, Appl
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C 135	14.6	66.4	1476	4	US-09-252-991A-15187	Sequence 15187, A	C 208	14.4	65.5	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 136	14.6	66.4	1521	2	US-09-004-502-2	Sequence 2, Appl	C 209	14.4	65.5	1664976	4	US-09-692-570-1	Sequence 1, Appl
C 137	14.6	66.4	1521	3	US-09-360-125-2	Sequence 2, Appl	C 210	14.2	64.5	111	2	US-09-174-060-8	Sequence 8, Appl
C 138	14.6	66.4	1521	4	US-09-914-81A-14	Sequence 14, Appl	C 211	14.2	64.5	111	2	US-09-174-060-8	Sequence 8, Appl
C 139	14.6	66.4	1560	4	US-09-270-767-11208	Sequence 11208, A	C 212	14.2	64.5	111	3	US-08-338-382-8	Sequence 8, Appl
C 140	14.6	66.4	1713	4	US-09-252-991A-14948	Sequence 14948, A	C 213	14.2	64.5	111	3	US-08-338-382-8	Sequence 8, Appl
C 141	14.6	66.4	1797	4	US-09-252-991A-14444	Sequence 14444, A	C 214	14.2	64.5	111	4	US-09-345-264-8	Sequence 8, Appl
C 142	14.6	66.4	1800	4	US-09-737-698B-29	Sequence 29, Appl	C 215	14.2	64.5	111	4	US-09-345-264-9	Sequence 9, Appl
C 143	14.6	66.4	1800	4	US-09-737-698B-29	Sequence 29, Appl	C 216	14.2	64.5	115	4	US-09-270-767-2055	Sequence 2055, Appl
C 144	14.6	66.4	1890	4	US-09-270-767-10215	Sequence 10215, A	C 217	14.2	64.5	127	4	US-09-270-767-17337	Sequence 17337, A
C 145	14.6	66.4	2025	4	US-09-252-991A-14929	Sequence 14929, A	C 218	14.2	64.5	217	4	US-09-335-011-12	Sequence 12, Appl
C 146	14.6	66.4	2025	4	US-09-270-767-10213	Sequence 10213, A	C 219	14.2	64.5	221	4	US-09-313-994A-5438	Sequence 5438, Ap
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C 466 13.8 62.7 570 3 US-08-998-416-792 Sequence 792, App
C 467 13.8 62.7 573 3 US-08-672-213-11 Sequence 11, Appl1
C 468 13.8 62.7 585 4 US-09-481-620A-9 Sequence 9, Appl1
C 469 13.8 62.7 585 4 US-09-621-976-16224 Sequence 16224, A
C 470 13.8 62.7 656 4 US-09-252-991A-14696 Sequence 14696, A
C 471 13.8 62.7 656 4 US-09-252-991A-4236 Sequence 4236, App
C 472 13.8 62.7 656 3 US-09-328-111-313 Sequence 113, App
C 473 13.8 62.7 664 4 US-09-352-991A-406 Sequence 406, App
C 474 13.8 62.7 705 4 US-09-252-991A-412 Sequence 412, App
C 475 13.8 62.7 705 4 US-09-252-991A-600 Sequence 600, App
C 476 13.8 62.7 711 4 US-09-270-767-11523 Sequence 11523, A
C 477 13.8 62.7 756 3 US-09-175-014-1 Sequence 1, Appl1
C 478 13.8 62.7 756 4 US-09-221-017B-723 Sequence 723, App
C 479 13.8 62.7 771 4 US-09-252-991A-4440 Sequence 4440, App
C 480 13.8 62.7 773 4 US-09-489-039A-7057 Sequence 7057, Ap
C 481 13.8 62.7 800 4 US-09-621-976-2725 Sequence 2725, Ap
C 482 13.8 62.7 888 3 US-09-227-357-56 Sequence 56, Appl
C 483 13.8 62.7 1044 4 US-09-270-767-27161 Sequence 27161, A
C 484 13.8 62.7 1065 4 US-09-252-991A-10622 Sequence 10622, A
C 485 13.8 62.7 1068 4 US-09-252-991A-438 Sequence 438, App
C 486 13.8 62.7 1089 4 US-09-252-991A-7838 Sequence 7838, App
C 487 13.8 62.7 1137 4 US-09-252-991A-7728 Sequence 7728, App
C 488 13.8 62.7 1164 4 US-09-252-991A-363 Sequence 363, Appl
C 489 13.8 62.7 1237 2 US-08-903-800A-1 Sequence 1, Appl1
C 490 13.8 62.7 1347 4 US-09-252-991A-367 Sequence 367, App
C 491 13.8 62.7 1374 3 US-09-411-687A-24 Sequence 24, Appl
C 492 13.8 62.7 1386 4 US-09-270-767-11648 Sequence 11648, A
C 493 13.8 62.7 1444 4 US-09-799-451-274 Sequence 274, App
C 494 13.8 62.7 1488 4 US-09-252-991A-4168 Sequence 4168, App
C 495 13.8 62.7 1500 3 US-09-174-768-3 Sequence 3, Appl1
C 496 13.8 62.7 1503 4 US-09-252-991A-4643 Sequence 4643, App
C 497 13.8 62.7 1566 4 US-09-799-451-273 Sequence 273, App
C 498 13.8 62.7 1656 4 US-09-602-487A-667 Sequence 667, App
C 499 13.8 62.7 1660 4 US-09-270-767-11561 Sequence 11561, A
C 500 13.8 62.7 1735 4 US-09-799-451-902 Sequence 902, App

```

## ALIGNMENTS

```

RESULT 1
US-10-140-002-405/c
Sequence 405, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Deenoys, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Geo, Wei-Oiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330P1C9
CURRENT APPLICATION NUMBER: US/10/140,002
PRIORITY FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 405
LENGTH: 3819
TYPE: DNA
ORGANISM: Homo Sapien

```

US-10-140-002-405

Query Match 95.5%; Score 21; DB 4; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 0.79;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGAGTTCTCGATGAGAT 21  
Db 399 TCGAGTTCTCGATGAGAT 379

RESULT 2

US-09-252-991A-10248

; Sequence 10248, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10248  
; LENGTH: 441  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10248

Query Match 74.5%; Score 16.4; DB 4; Length 441;  
Best Local Similarity 94.4%; Pred. No. 89;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAGTTCTCGATGAG 19  
Db 274 TCGAGTTCTCGATGAG 291

RESULT 3

US-09-252-991A-10461  
; Sequence 10461, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10461  
; LENGTH: 1659  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10461

Query Match 74.5%; Score 16.4; DB 4; Length 1659;  
Best Local Similarity 94.4%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAGTTCTCGATGAG 19  
Db 803 TCGAGTTCTCGATGAG 820

RESULT 4

US-09-252-991A-10707/c  
; Sequence 10707, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 10707  
; LENGTH: 3267  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-10707

Query Match 74.5%; Score 16.4; DB 4; Length 3267;  
Best Local Similarity 94.4%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAGTTCTCGATGAG 19  
Db 758 TCGAGTTCTCGATGAG 741

RESULT 5

US-09-252-991A-14488/c  
; Sequence 14488, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14488  
; LENGTH: 519  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14488

Query Match 73.6%; Score 16.2; DB 4; Length 519;  
Best Local Similarity 85.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAGTTCTCGATGAGATC 22  
Db 234 TCGAGTTCTCGAGATC 214

RESULT 6

US-09-252-991A-15133  
; Sequence 15133, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 15133  
LENGTH: 1347  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15133

Query Match 73.6%; Score 16.2; DB 4; Length 1347;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGGAGATC 22  
DB 788 TCGAGTTCTCGCGGAAGATC 808

RESULT 7  
US-09-252-991A-14625/c  
Sequence 14625, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14625  
LENGTH: 1359  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14625

Query Match 73.6%; Score 16.2; DB 4; Length 1359;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGGAGATC 22  
DB 578 TCGAGTTCTCGCGGAAGATC 558

RESULT 8  
US-09-252-991A-15137/c  
Sequence 15137, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 15137  
LENGTH: 1446  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15137

Query Match 73.6%; Score 16.2; DB 4; Length 1446;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCTCGATGGAGATC 22  
DB 1010 TCGAGTTCTCGAAGTCGATC 990

RESULT 9  
US-09-689-012-1/c  
Sequence 1, Application US/09689012  
Patent No. 6670135  
GENERAL INFORMATION:  
APPLICANT: Spri998, Melanie K.  
TITLE OF INVENTION: NOVEL SEMAPHORIN POLYPEPTIDES  
FILE REFERENCE: 2634-US  
CURRENT APPLICATION NUMBER: US/09/689,012  
CURRENT FILING DATE: 2000-10-12  
PRIOR APPLICATION NUMBER: PCT/US99/09831  
PRIOR FILING DATE: 1999-05-05  
PRIOR APPLICATION NUMBER: US 60/085,497  
PRIOR FILING DATE: 1998-05-14  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 2001  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2001)  
OTHER INFORMATION:  
US-09-689-012-1

Query Match 73.6%; Score 16.2; DB 4; Length 2001;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGGAGAT 21  
DB 1575 TTCGAGTTCTCGATGGAGAT 1555

RESULT 10  
US-09-240-410-1/c  
Sequence 1, Application US/09240410  
Patent No. 6197544  
GENERAL INFORMATION:  
APPLICANT: MICHALOVICH, DAVID  
APPLICANT: HAYES, PHILIP DAVID  
TITLE OF INVENTION: NOVEL COMPOUNDS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,410  
FILING DATE: 27-JAN-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK APPLICATION NO. TO BE ASSIGNED  
FILING DATE: 20-JAN-1999  
APPLICATION NUMBER: EP APPLICATION NO. 98300694.1

FILING DATE: 30-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GP-30039  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0700  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2010 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-240-410-1

Query Match 73.6%; Score 16.2; DB 3; Length 2010;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21  
|||||  
Db 1575 TTCGAGCTGTAGATGAGAT 1555

RESULT 11  
US-09-252-991A-14624  
Sequence 14624, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14624  
LENGTH: 2154  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14624

Query Match 73.6%; Score 16.2; DB 4; Length 2154;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCGAGTCTCGATGAGATC 22  
|||||  
Db 482 TTCGAGTCTCGAAGTCGATC 502

RESULT 12  
US-09-041-236-1/c  
Sequence 1, Application US/09041236  
Patent No. 6225285  
GENERAL INFORMATION:  
APPLICANT: Luo, Yuling  
APPLICANT: Xiomel, Xu  
TITLE OF INVENTION: Semaphorin K1  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA

ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,236  
FILING DATE: March 11, 1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: EXEL98-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2498 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1902  
US-09-041-236-1

Query Match 73.6%; Score 16.2; DB 3; Length 2498;  
Best Local Similarity 85.7%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21  
|||||  
Db 1479 TTCGAGCTGTAGATGAGAT 1459

RESULT 13  
US-09-771-467C-1/c  
Sequence 1, Application US/09771467C  
Patent No. 6583277  
GENERAL INFORMATION:  
APPLICANT: Luo, Yuling  
APPLICANT: Xiomel, Xu  
TITLE OF INVENTION: Semaphorin K1 Polypeptides  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/771,467C  
FILING DATE: 26-Jan-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: EXEL98-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2498 base pairs

```

;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1902
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-771-467C-1

Query Match      73.6%; Score 16.2; DB 4; Length 2498;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TTGGAGTTCTCGATGAGATC 21
Db      1479 TTGGAGCTGTATGATGAGAT 1459

RESULT 14
US-09-252-991A-15001/C
; Sequence 15001, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15001
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15001

Query Match      73.6%; Score 16.2; DB 4; Length 2622;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TTGGAGTTCTCGATGAGATC 22
Db      957 TTGGAGTTCTCGATGAGATC 937

RESULT 15
US-09-669-751-133
; Sequence 133, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669,751
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-133

Query Match      71.8%; Score 15.8; DB 4; Length 550;
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```

;
; Best Local Similarity 89.5%; Pred. No. 1.8e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TTGGAGTTCTCGATGAG 19
Db      272 TTGGAGTTCTCGATGAGCG 290

RESULT 16
US-09-270-767-14247
; Sequence 14247, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14247
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14247

Query Match      71.8%; Score 15.8; DB 4; Length 636;
Best Local Similarity 89.5%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TTGGAGTTCTCGATGAG 19
Db      272 TTGGAGTTCTCGATGAGCG 290

RESULT 17
US-09-248-796A-414/C
; Sequence 414, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Ketch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 414
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-414

Query Match      71.8%; Score 15.8; DB 4; Length 744;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 GGAGTTCTCGATGAGATC 22
Db      704 GGAGTTCTCGATGAGATC 686

RESULT 18
US-09-270-767-11307/C
; Sequence 11307, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
```



FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 11307  
LENGTH: 1586  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-11307

Query Match 71.8%; Score 15.8; DB 4; Length 1586;  
Best Local Similarity 89.5%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAGTTCTCGATGAGATC 22  
DB 1315 GGCGTTCTCGATGATGATC 1297

RESULT 19  
US-09-252-991A-6042  
Sequence 6042, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 6042  
LENGTH: 1836  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6042

Query Match 71.8%; Score 15.8; DB 4; Length 1836;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAGTTCTCGATGAGATC 22  
DB 723 GGAGTTCTCGATGAGATC 741

RESULT 20  
US-09-252-991A-6258/C  
Sequence 6258, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 6258  
LENGTH: 1911  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6258

Query Match 71.8%; Score 15.8; DB 4; Length 1911;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAGTTCTCGATGAGATC 22  
DB 1156 GGAGTTCTCGATGAGATC 1138

RESULT 21  
US-09-016-434-320/C  
Sequence 320, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: 71-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 320:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: HMT3A2T01  
CLONE: 1854243  
US-09-016-434-320

Query Match 70.9%; Score 15.6; DB 4; Length 251;  
Best Local Similarity 81.8%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTGGAGTTCTCGATGAGATC 22  
DB 96 TTGGAGTTCTCGATGAGATC 75

RESULT 22  
US-09-328-352-3744  
Sequence 3744, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

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; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3744
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3744

Query Match      70.3%; Score 15.6; DB 4; Length 393;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTGGAGTCTCGATGAGATC 22
DB      249 TTCAAGTCTCGATGAGATC 270

RESULT 23
US-09-602-787A-199/C
; Sequence 199, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schöder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habermann, Gregor
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3

```

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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 199
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1072)
; OTHER INFORMATION: RXA02269
US-09-602-787A-199

Query Match      70.9%; Score 15.6; DB 4; Length 1095;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTGGAGTCTCGATGAGATC 22
DB      140 TTGGAGTCTCGGCGAGATC 119

RESULT 24
US-09-492-709A-196/C
; Sequence 196, Application US/09492709A
; Patent No. 6720139
; GENERAL INFORMATION:
; APPLICANT: Zykkind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; FILE REFERENCE: ELITRA.001A
; CURRENT APPLICATION NUMBER: US/09/492,709A
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0

```

SEQ ID NO 196  
LENGTH: 1371  
TYPE: DNA  
ORGANISM: E. Coli  
US-09-492-709A-196

Query Match 70.9%; Score 15.6; DB 4; Length 1371;  
Best Local Similarity 81.8%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGATC 22  
|||||  
Db 933 TTCGAGTTCTCGATGAGATC 912  
|||||

RESULT 25  
US-09-799-875-3/c  
Sequence 3, Application US/09799875  
Patent No. 6638721  
GENERAL INFORMATION:  
APPLICANT: Meyers, Rachel  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: Williamson, Mark

TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses  
TITLE OF INVENTION: Therefor  
FILE REFERENCE: 35800/209996  
CURRENT FILING DATE: 2001-03-06  
PRIOR APPLICATION NUMBER: 60/182,059  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 09/659,287  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3

LENGTH: 2637  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-799-875-3

Query Match 70.9%; Score 15.6; DB 4; Length 2637;  
Best Local Similarity 81.8%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGATC 22  
|||||  
Db 2171 TTCGAGTTCTCGATGAGATC 2150  
|||||

RESULT 26  
US-09-799-875-1/c  
Sequence 1, Application US/09799875  
Patent No. 6638721  
GENERAL INFORMATION:  
APPLICANT: Meyers, Rachel  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: Williamson, Mark  
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses  
TITLE OF INVENTION: Therefor  
FILE REFERENCE: 35800/209996  
CURRENT FILING DATE: US/09/799,875  
PRIOR APPLICATION NUMBER: 2001-03-06  
PRIOR FILING DATE: 60/182,059  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: 09/659,287  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 3003  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: CDS  
LOCATION: (52)...(2688)  
US-09-799-875-1

Query Match 70.9%; Score 15.6; DB 4; Length 3003;  
Best Local Similarity 81.8%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGATC 22  
|||||  
Db 2222 TTCGAGTTCTCGATGAGATC 2201  
|||||

RESULT 27  
US-08-311-731A-123/c  
Sequence 123, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36470 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULAR TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LAPRAE  
US-08-311-731A-123

Query Match 70.9%; Score 15.6; DB 4; Length 36470;  
Best Local Similarity 81.8%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGATC 22  
|||||  
Db 17340 TACGTACTCTCGATGAGATC 17319  
|||||

RESULT 28  
US-09-410-551B-1/c  
Sequence 1, Application US/09410551B  
Patent No. 6503737

```

; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTU, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
; FILE REFERENCE: 30062-20026.00
; CURRENT APPLICATION NUMBER: US/09/410,551B
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-410-551B-1

Query Match          70.9%; Score 15.6; DB 4; Length 77536;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTGGAGTTCTCGATGAGATC 22
DB      55028 TTGGCGATCTCGACGAGACC 55007

RESULT 29
US-09-940-316B-1/c
; Sequence 1, Application US/09940316B
; Patent No. 6759536
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTU, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275)...(71465)
US-09-940-316B-1
```

```

Query Match          70.9%; Score 15.6; DB 4; Length 77536;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TTGGAGTTCTCGATGAGATC 22
DB      55028 TTGGCGATCTCGACGAGACC 55007

RESULT 30
US-09-799-451-327
; Sequence 327, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Rylye
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Keena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_Fl_genes Version 2.0
; SEQ ID NO 327
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (355)..(1683)
US-09-799-451-327

Query Match          70.0%; Score 15.4; DB 4; Length 1686;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GGAGTTCTCGATGAGAGA 20
DB      1335 GGAGTTCTCGATGAGAGA 1351

RESULT 31
US-09-377-466B-9/c
; Sequence 9, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21 (15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: non-naturally  
OTHER INFORMATION: occurring nucleotide sequence encoding a Cry3Bb  
OTHER INFORMATION: variant 11231mw1 amino acid sequence  
NAME/KEY: CDS  
LOCATION: (3)..(1961)  
OTHER INFORMATION: coding sequence for a Cry3Bb variant 11231mw1  
OTHER INFORMATION: amino acid sequence  
US-09-377-466B-9

Query Match 70.0%; Score 15.4; DB 4; Length 1984;  
Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTCTCGATGAGA 20  
DB 989 GGAGTCTCGATGAGA 973

RESULT 32  
US-09-377-466B-11/c  
Sequence 11, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 11  
LENGTH: 1984  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: non-naturally  
OTHER INFORMATION: occurring nucleotide sequence encoding a Cry3Bb  
OTHER INFORMATION: variant 11231mw2 amino acid sequence  
NAME/KEY: CDS  
LOCATION: (3)..(1961)  
OTHER INFORMATION: coding sequence for a Cry3Bb variant 11231mw2  
OTHER INFORMATION: amino acid sequence  
US-09-377-466B-11

Query Match 70.0%; Score 15.4; DB 4; Length 1984;  
Best Local Similarity 94.1%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTCTCGATGAGA 20  
DB 989 GGAGTCTCGATGAGA 973

RESULT 33  
US-09-377-466B-19/c  
Sequence 19, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 19  
LENGTH: 3039  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette

NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CamV,AS4  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcd1  
NAME/KEY: Intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
NAME/KEY: CDS  
LOCATION: (811)..(2769)  
OTHER INFORMATION: Cry3Bb1 variant 11231mw1  
NAME/KEY: terminator  
LOCATION: (2787)..(3020)  
OTHER INFORMATION: T-Ta.hsp17  
US-09-377-466B-19

Query Match 70.0%; Score 15.4; DB 4; Length 3039;  
Best Local Similarity 94.1%; Pred. No. 3.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTCTCGATGAGA 20  
DB 1797 GGAGTCTCGATGAGA 1781

RESULT 34  
US-09-377-466B-21/c  
Sequence 21, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 21  
LENGTH: 3039  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette  
NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CamV,AS4  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcd1  
NAME/KEY: Intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
NAME/KEY: CDS  
LOCATION: (811)..(2769)  
OTHER INFORMATION: Cry3Bb1 variant 11231mw2  
NAME/KEY: terminator  
LOCATION: (2787)..(3020)  
OTHER INFORMATION: T-Ta.hsp17  
US-09-377-466B-21

Query Match 70.0%; Score 15.4; DB 4; Length 3039;  
Best Local Similarity 94.1%; Pred. No. 3.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGTCTCGATGAGA 20  
DB 1797 GGAGTCTCGATGAGA 1781

RESULT 35  
US-09-377-466B-17/c

```
Sequence 17, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 3450
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
NAME/KEY: Promoter
LOCATION: (14)..(235)
OTHER INFORMATION: P-CaMV.AS4
NAME/KEY: 5'UTR
LOCATION: (240)..(304)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: Intron
LOCATION: (318)..(805)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: transic peptide
LOCATION: (825)..(971)
OTHER INFORMATION: amino terminal TS-Zm.rbcs
NAME/KEY: Intron
LOCATION: (972)..(1134)
OTHER INFORMATION: I-Zm.rbcs
NAME/KEY: transic peptide
LOCATION: (1135)..(1221)
OTHER INFORMATION: carboxy terminus TS-Zm.rbcs
NAME/KEY: CDS
LOCATION: (1222)..(3180)
OTHER INFORMATION: Cry3Bb1 variant 11231mv1
NAME/KEY: terminator
LOCATION: (3198)..(3431)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-17

Query Match          70.0%; Score 15.4; DB 4; Length 3450;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 4 GGAGTTCTCGATGAGCA 20
Db 2208 GGAGTTCTCGATGAGCA 2192

RESULT 36
US-09-377-466B-23/c
Sequence 23, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 3469
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
NAME/KEY: Promoter
LOCATION: (25)..(640)
```

```
OTHER INFORMATION: P-CaMV.35S
NAME/KEY: 5'UTR
LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcb1
NAME/KEY: Intron
LOCATION: (746)..(1238)
OTHER INFORMATION: I-Os.Act1
NAME/KEY: CDS
LOCATION: (1241)..(3199)
OTHER INFORMATION: Cry3Bb1 variant 11231mv2
NAME/KEY: terminator
LOCATION: (3217)..(3450)
OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-23

Query Match          70.0%; Score 15.4; DB 4; Length 3469;
Best Local Similarity 94.1%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 4 GGAGTTCTCGATGAGCA 20
Db 2227 GGAGTTCTCGATGAGCA 2211

RESULT 37
US-08-637-759B-8/c
Sequence 8, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPLMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Partial sequence of Salmonella typhimurium
US-08-637-759B-8
```



Query Match 69.1%; Score 15.2; DB 2; Length 300;  
Best Local Similarity 85.0%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAGTTCTCGATGAGATC 22  
Db 39 CGAGTTATCGATGACGACC 20

## RESULT 38

US-08-871-355A-8/c  
; Sequence 8, Application US/08871355A  
; Patent No. 6015669  
GENERAL INFORMATION:  
APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,355A  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/02875  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPLMS 101 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Partial sequence of *Salmonella typhimurium*  
US-08-871-355A-8

Query Match 69.1%; Score 15.2; DB 3; Length 300;  
Best Local Similarity 85.0%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAGTTCTCGATGAGATC 22  
Db 39 CGAGTTATCGATGACGACC 20

RESULT 39  
US-09-201-945-8/c  
; Sequence 8, Application US/09201945  
; Patent No. 6342215

GENERAL INFORMATION:  
APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,945  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/637,759  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPLMS 101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8795  
TELEFAX: (404) 873-8794  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Partial sequence of *Salmonella typhimurium*  
US-09-201-945-8

Query Match 69.1%; Score 15.2; DB 3; Length 300;  
Best Local Similarity 85.0%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAGTTCTCGATGAGATC 22  
Db 39 CGAGTTATCGATGACGACC 20

RESULT 40  
US-09-621-976-15382/c  
; Sequence 15382, Application US/09621976  
; Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 15382  
LENGTH: 413  
TYPE: DNA  
ORGANISM: *Homo sapiens*

US-09-621-976-15382

Query Match 69.1%; Score 15.2; DB 4; Length 413;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAGA 20  
DB 389 TTGGCAGTTCTCGAAGAGAGA 370

RESULT 41

US-09-513-999C-12831/c  
; Sequence 12831, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclercq, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24, 487  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 12831  
; LENGTH: 565  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 391  
; OTHER INFORMATION: m=a or c  
US-09-513-999C-12831

Query Match 69.1%; Score 15.2; DB 4; Length 565;  
Best Local Similarity 85.0%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAGA 20  
DB 363 TTGGCAGTTCTCGAAGAGAGA 344

RESULT 42

US-09-270-767-2463/c  
; Sequence 2463, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2463  
; LENGTH: 621  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: n means any nucleotide  
US-09-270-767-2463

Query Match 69.1%; Score 15.2; DB 4; Length 621;  
Best Local Similarity 85.0%; Pred. No. 3.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGAGGTTCTCGATGAGATC 22  
DB 363 TTGGCAGTTCTCGAAGAGAGA 344

DB 470 CGGACTTCTCGATCGGAGATC 451

RESULT 43

US-09-270-767-17745/c  
; Sequence 17745, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 17745  
; LENGTH: 621  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: n means any nucleotide  
US-09-270-767-17745

Query Match 69.1%; Score 15.2; DB 4; Length 621;  
Best Local Similarity 85.0%; Pred. No. 3.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGGAGTTCTCGATGAGATC 22  
DB 470 CGGACTTCTCGATCGGAGATC 451

RESULT 44

US-09-513-999C-1940/c  
; Sequence 1940, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclercq, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1940  
; LENGTH: 690  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 310..690  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 508  
; OTHER INFORMATION: n=a, g, c or t  
; FEATURE:  
; NAME/KEY: UNSURB  
; LOCATION: 67  
; OTHER INFORMATION: Xaa=Asp or His or Asn or Tyr  
US-09-513-999C-1940

Query Match 69.1%; Score 15.2; DB 4; Length 690;  
Best Local Similarity 85.0%; Pred. No. 3.6e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAGA 20  
DB 363 TTGGCAGTTCTCGAAGAGAGA 344

RESULT 45  
US-09-602-787A-61  
Sequence 61, Application US/09602787A  
Patent No. 6696561  
GENERAL INFORMATION:  
APPLICANT: Pompeius, Mark  
APPLICANT: Krüger, Burthard  
APPLICANT: Schöder, Hartwig  
APPLICANT: Zelder, Oskar  
APPLICANT: Habeshauer, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
FILE REFERENCE: BGI-125CP  
CURRENT APPLICATION NUMBER: US/09/602,787A  
CURRENT FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: USN 60/141031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: DE 19931454.3  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931478.0  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931563.9  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932122.1  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932124.8  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932125.6  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932180.9  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932182.5  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932190.6  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932191.4  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932209.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932212.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932227.9  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932228.7  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932229.5  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932230.9  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932927.3  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933005.0  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933006.9  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19940764.9  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940765.7  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940766.5  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940830.0  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940831.9  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940832.7  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19940833.5

PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19941378.9  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941379.7  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941395.9  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19942077.7  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: DE 19942078.5  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: DE 19942079.3  
PRIOR FILING DATE: 1999-09-03  
PRIOR APPLICATION NUMBER: DE 19942088.2  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 678  
SEQ ID NO 61  
LENGTH: 1047  
TYPE: DNA  
ORGANISM: Corynebacterium glutamicum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (101)..(1024)  
OTHER INFORMATION: RXA01060  
US-09-602-787A-61

Query Match 69.1%; Score 15.2; DB 4; Length 1047;  
Best Local Similarity 85.0%; Pred. No. 3.8e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CGGAGTCTCGATCGAGATC 22  
DB 643 CGGAGATCTTGATCGAGATC 662

RESULT 46  
US-09-146-675-2  
Sequence 2, Application US/09146675B  
Patent No. 6048731  
GENERAL INFORMATION:  
APPLICANT: Kong, Huimin  
APPLICANT: Higgins S., Lauren  
APPLICANT: Dalton A., Michael  
TITLE OF INVENTION: Method For Cloning And Producing The SgrAI Restriction  
FILE REFERENCE: SgrAI  
CURRENT APPLICATION NUMBER: US/09/146,675B  
CURRENT FILING DATE: 1998-09-03  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1290  
TYPE: DNA  
ORGANISM: Streptomyces griseus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1287)  
US-09-146-675-2

Query Match 69.1%; Score 15.2; DB 3; Length 1290;  
Best Local Similarity 85.0%; Pred. No. 4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTCGAGTTCTCGATCGAGA 20  
DB 592 TTCGCGCTTCGCGATGGGA 611

RESULT 47  
US-09-252-991A-9857/C  
Sequence 9857, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9857  
LENGTH: 1722  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9857

Query Match 69.1%; Score 15.2; DB 4; Length 1722;  
Best Local Similarity 85.0%; Pred. No. 4.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCGATGAGAT 21  
DB 1616 TCGCGATTCGATGAGAT 1597

RESULT 48  
US-09-548-938A-4/C  
Sequence 4, Application US/09548938A  
Patent No. 6573086  
GENERAL INFORMATION:  
APPLICANT: EMALFAR, MARK AARON  
APPLICANT: BURLINGAME, RICHARD PAUL  
APPLICANT: OLSON, PHILIP TERRY  
APPLICANT: SINITSYN, ARKADY PANTELEIMONOVICH  
APPLICANT: BOUSSON, JEAN CHRISTOPHE  
APPLICANT: PYNNONE, CHRISTINE MARIE  
APPLICANT: PUNT, PETER JAN  
APPLICANT: VAN-ZEIJL, CORNELIA MARIA JOHANNA  
TITLE OF INVENTION: TRANSFORMATION SYSTEM IN THE FIELD OF FILAMENTOUS FUNGI  
FILE REFERENCE: 3123-4001  
CURRENT APPLICATION NUMBER: US/09/548,938A  
CURRENT FILING DATE: 2000-04-13  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 2547  
TYPE: DNA  
ORGANISM: Chrysoosporium lucknowense  
US-09-548-938A-4

Query Match 69.1%; Score 15.2; DB 4; Length 2547;  
Best Local Similarity 85.0%; Pred. No. 4.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TCGAGTTCGATGAGAT 21  
DB 1632 TCGAGTTCGATGAGAT 1613

RESULT 49  
US-09-112-580-5/C  
Sequence 5, Application US/09112580  
Patent No. 6610539  
GENERAL INFORMATION:  
APPLICANT: WRIGHT, Jim A.  
APPLICANT: YOUNG, Aiding  
APPLICANT: DUCOURD, Dominique  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF  
FILE REFERENCE: 032396-016  
CURRENT APPLICATION NUMBER: US/09/112,580

CURRENT FILING DATE: 1998-07-09  
EARLIER APPLICATION NUMBER: US 60/052,160  
EARLIER FILING DATE: 1997-07-10  
NUMBER OF SEQ ID NOS: 265  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 3811  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-112-580-5

Query Match 69.1%; Score 15.2; DB 4; Length 3811;  
Best Local Similarity 85.0%; Pred. No. 4.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 2209 TCGATTTTCGATGAGAT 2190

RESULT 50  
US-09-302-626B-59/C  
Sequence 59, Application US/09302626B  
Patent No. 6709660  
GENERAL INFORMATION:  
APPLICANT: Scalato, Enzo  
APPLICANT: Maignani, Vega  
APPLICANT: Rappuoli, Rino  
APPLICANT: Pizzo, Mariagrazia  
APPLICANT: Grandi, Guido  
TITLE OF INVENTION: Meningococcal Antigens  
FILE REFERENCE: CHIR0159  
CURRENT APPLICATION NUMBER: US/09/302,626B  
CURRENT FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: PCT/IB99/00103  
PRIOR FILING DATE: 1999-01-14  
NUMBER OF SEQ ID NOS: 195  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 59  
LENGTH: 5937  
TYPE: DNA  
ORGANISM: Neisseria meningitidis  
US-09-302-626B-59

Query Match 69.1%; Score 15.2; DB 4; Length 5937;  
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Search completed: February 2, 2005, 01:35:44  
Job time: 112 secs

GenCore version 5.1.6  
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CM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 23:49:03 ; Search time 418 Seconds

(without alignments)  
302.415 Million cell updates/sec

Title: US-10-073-054-14

Perfect score: 22

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues 8600550

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Listing first 500 summaries

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Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 156	21	95.5	3819	14	US-10-128-690A-405	Sequence 405, App	C 229	21	95.5	3819	14	US-10-219-528-133	Sequence 133, App
C 157	21	95.5	3819	14	US-10-128-691A-405	Sequence 405, App	C 230	21	95.5	3819	14	US-10-219-528-133	Sequence 133, App
C 158	21	95.5	3819	14	US-10-131-819A-405	Sequence 405, App	C 231	21	95.5	3819	14	US-10-227-880-133	Sequence 133, App



[illegible]

C 378	21	95.5	3819	15	US-10-145-747-405
C 379	21	95.5	3819	15	US-10-145-752-405
C 380	21	95.5	3819	15	US-10-145-754-405
C 381	21	95.5	3819	15	US-10-145-755-405
C 382	21	95.5	3819	15	US-10-145-758-405
C 383	21	95.5	3819	15	US-10-145-820-405
C 384	21	95.5	3819	15	US-10-145-820-405
C 385	21	95.5	3819	15	US-10-145-873-405
C 386	21	95.5	3819	15	US-10-147-821-405
C 387	21	95.5	3819	15	US-10-147-882-405
C 388	21	95.5	3819	15	US-10-147-903-405
C 389	21	95.5	3819	15	US-10-147-922-405
C 390	21	95.5	3819	15	US-10-152-801-405
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C 392	21	95.5	3819	15	US-10-158-792-405
C 393	21	95.5	3819	15	US-10-158-862-405
C 394	21	95.5	3819	15	US-10-143-035-405
C 395	21	95.5	3819	15	US-10-145-751-405
C 396	21	95.5	3819	15	US-10-145-822-405
C 397	21	95.5	3819	15	US-10-145-824-405
C 398	21	95.5	3819	15	US-10-145-827-405
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C 401	21	95.5	3819	15	US-10-145-877-405
C 402	21	95.5	3819	15	US-10-145-888-405
C 403	21	95.5	3819	15	US-10-146-787-405
C 404	21	95.5	3819	15	US-10-146-790-405
C 405	21	95.5	3819	15	US-10-146-793-405
C 406	21	95.5	3819	15	US-10-147-480-405
C 407	21	95.5	3819	15	US-10-147-485-405
C 408	21	95.5	3819	15	US-10-147-486-405
C 409	21	95.5	3819	15	US-10-147-487-405
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C 411	21	95.5	3819	15	US-10-147-494-405
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C 414	21	95.5	3819	15	US-10-147-524-405
C 415	21	95.5	3819	15	US-10-152-379-405
C 416	21	95.5	3819	15	US-10-152-394-405
C 417	21	95.5	3819	15	US-10-152-406-405
C 418	21	95.5	3819	15	US-10-156-947-405
C 419	21	95.5	3819	15	US-10-157-778-405
C 420	21	95.5	3819	15	US-10-157-799-405
C 421	21	95.5	3819	15	US-10-160-504-405
C 422	21	95.5	3819	15	US-10-017-191A-48
C 423	21	95.5	3819	15	US-10-145-634-405
C 424	21	95.5	3819	15	US-10-147-520-405
C 425	21	95.5	3819	15	US-10-157-761-405
C 426	21	95.5	3819	15	US-10-176-989-405
C 427	21	95.5	3819	15	US-10-147-451-405
C 428	21	95.5	3819	15	US-10-152-378-405
C 429	21	95.5	3819	15	US-10-152-382-405
C 430	21	95.5	3819	15	US-10-152-383-405
C 431	21	95.5	3819	15	US-10-152-384-405
C 432	21	95.5	3819	15	US-10-152-387-405
C 433	21	95.5	3819	15	US-10-152-389-405
C 434	21	95.5	3819	15	US-10-152-390-405
C 435	21	95.5	3819	15	US-10-152-392-405
C 436	21	95.5	3819	15	US-10-152-403-405
C 437	21	95.5	3819	15	US-10-157-756-405
C 438	21	95.5	3819	15	US-10-157-784-405
C 439	21	95.5	3819	15	US-10-157-797-405

[illegible]

C 451	21	95.5	3819	15	US-10-146-789-405
C 452	21	95.5	3819	15	US-10-147-483-405
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C 454	21	95.5	3819	15	US-10-147-505-405
C 455	21	95.5	3819	15	US-10-147-516-405
C 456	21	95.5	3819	15	US-10-153-398-405
C 457	21	95.5	3819	15	US-10-153-398-405
C 458	21	95.5	3819	15	US-10-165-067A-48
C 459	21	95.5	3819	15	US-10-146-017A-48
C 460	21	95.5	3819	15	US-10-146-750-405
C 461	21	95.5	3819	15	US-10-152-373-405
C 462	21	95.5	3819	15	US-10-164-728A-48
C 463	21	95.5	3819	15	US-10-223-081-91
C 464	21	95.5	3819	15	US-10-218-765-133
C 465	21	95.5	3819	15	US-10-219-063-133
C 466	21	95.5	3819	15	US-10-219-066-133
C 467	21	95.5	3819	15	US-10-219-067-133
C 468	21	95.5	3819	15	US-10-219-068-133
C 469	21	95.5	3819	15	US-10-219-068-133
C 470	21	95.5	3819	15	US-10-219-073-133
C 471	21	95.5	3819	15	US-10-219-475-133
C 472	21	95.5	3819	15	US-10-219-480-133
C 473	21	95.5	3819	15	US-10-219-488-133
C 474	21	95.5	3819	15	US-10-219-528-133
C 475	21	95.5	3819	15	US-10-219-528-133
C 476	21	95.5	3819	15	US-10-219-530-133
C 477	21	95.5	3819	15	US-10-219-531-133
C 478	21	95.5	3819	15	US-10-219-532-133
C 479	21	95.5	3819	15	US-10-219-533-133
C 480	21	95.5	3819	15	US-10-230-437-133
C 481	21	95.5	3819	15	US-10-232-228-133
C 482	21	95.5	3819	15	US-10-013-926A-48
C 483	21	95.5	3819	15	US-10-165-247A-48
C 484	21	95.5	3819	15	US-10-145-124A-48
C 485	21	95.5	3819	15	US-10-160-502A-48
C 486	21	95.5	3819	15	US-10-121-044-405
C 487	21	95.5	3819	15	US-10-121-055-405
C 488	21	95.5	3819	15	US-10-121-057-405
C 489	21	95.5	3819	15	US-10-121-058-405
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C 491	21	95.5	3819	15	US-10-121-060-405
C 492	21	95.5	3819	15	US-10-123-109-405
C 493	21	95.5	3819	15	US-10-123-154-405
C 494	21	95.5	3819	15	US-10-123-157-405
C 495	21	95.5	3819	15	US-10-123-906-405
C 496	21	95.5	3819	15	US-10-124-814-405
C 497	21	95.5	3819	15	US-10-124-816-405
C 498	21	95.5	3819	15	US-10-124-820-405
C 499	21	95.5	3819	15	US-10-125-704-405
C 500	21	95.5	3819	18	US-10-145-825-405

[illegible]

ALIGNMENTS

RESULT 1  
US-10-073-054-14  
; Sequence 14, Application US/10073054  
; Publication No. US20030167485A1  
GENERAL INFORMATION:  
APPLICANT: Garvan Institute of Medical Research  
APPLICANT: HERZOG, Herbert  
TITLE OF INVENTION: No. US20030167485A1 G-protein coupled, receptor-encoding gene  
TITLE OF INVENTION: therefor  
FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
CURRENT APPLICATION NUMBER: US/10/073,054  
CURRENT FILING DATE: 2002-02-12  
PRIOR APPLICATION NUMBER: 09/308,696  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00805  
PRIOR FILING DATE: 1996-09-24  
PRIOR APPLICATION NUMBER: AU P09386  
PRIOR FILING DATE: 1997-09-24

NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 14  
 LENGTH: 22  
 TYPE: DNA  
 ORGANISM: probe  
 US-10-073-054-14

Query Match 100.0%; Score 22; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.59; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0;

Qy 1 TTCGAGTCTCGATGAGATC 22  
 Db 1 TTCGAGTCTCGATGAGATC 22

RESULT 2  
 US-10-073-054-11/c

Sequence 11, Application US/10073054  
 Publication No. US20030167485A1  
 GENERAL INFORMATION:

APPLICANT: Gartner Institute of Medical Research  
 APPLICANT: HERZOG, Herbert  
 TITLE OF INVENTION: No. US20030167485A1 G-protein coupled receptor-encoding gene an

FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
 CURRENT APPLICATION NUMBER: US/10/073,054

PRIOR FILING DATE: 2002-02-12  
 PRIOR APPLICATION NUMBER: US 09/308,696

PRIOR FILING DATE: 1999-06-11  
 PRIOR APPLICATION NUMBER: PCT/AU98/00805

PRIOR FILING DATE: 1998-09-24  
 PRIOR APPLICATION NUMBER: AU P09386

PRIOR FILING DATE: 1997-09-24  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: PatentIn version 3.1

SEQ ID NO: 11  
 LENGTH: 22  
 TYPE: DNA  
 ORGANISM: probe  
 US-10-073-054-11

Query Match 95.5%; Score 21; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;  
 Matches 21; Conservative 0;

Qy 1 TTCGAGTCTCGATGAGAT 21  
 Db 22 TTCGAGTCTCGATGAGAT 2

RESULT 3  
 US-09-864-761-25383/c

Sequence 25383, Application US/09864761  
 Patent No. US20020048763A1  
 GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761  
 PRIOR FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 09/608,408  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 49117  
 SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1

SEQ ID NO: 25383  
 LENGTH: 423  
 TYPE: DNA  
 ORGANISM: Homo sapiens

FEATURE:  
 OTHER INFORMATION: MAP TO AC018552.2  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.7  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.8  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.3  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2  
 OTHER INFORMATION: SWISSPROT HIT: P28984, EVALUATE 3.70e-01

OTHER INFORMATION: NT HIT: A011001.1, EVALUATE 0.00e+00  
 OTHER INFORMATION: EST\_HUMAN HIT: A1046540.1, EVALUATE 0.00e+00

US-09-864-761-25383  
 Query Match 95.5%; Score 21; DB 9; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 21; Conservative 0;

Qy 1 TTCGAGTCTCGATGAGAT 21  
 Db 122 TTCGAGTCTCGATGAGAT 102

RESULT 4  
 US-09-814-353-14450/c

Sequence 14450, Application US/09814353  
 Publication No. US2003016583A1  
 GENERAL INFORMATION:

APPLICANT: Lee, John  
 APPLICANT: Thompson, Pamela  
 APPLICANT: Lallie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
 IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER  
 FILE REFERENCE: MRI-0068  
 CURRENT APPLICATION NUMBER: US/09/814,353

PRIOR FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: US 09/814,353

PRIOR FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: US 09/814,353

PRIOR APPLICATION NUMBER: US 60/191,031  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/207,124  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 60/211,940  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: US 60/216,820  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: US 60/220,661  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/251,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14450  
LENGTH: 493  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-814-353-14450

Query Match 95.5%; Score 21; DB 10; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 416 TTCGAGTTCTCGATGAGAT 396

RESULT 5  
US-10-723-860-3391/c  
Sequence 3391, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Zlotnick, Albert M.  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
FILE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
PRIOR FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3391  
LENGTH: 527  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-723-860-3391

Query Match 95.5%; Score 21; DB 18; Length 527;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 247 TTCGAGTTCTCGATGAGAT 227

RESULT 6  
US-09-864-761-8712/c  
Sequence 8712, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wenheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 8712  
LENGTH: 582  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC018552.2  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.7  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.4  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2  
US-09-864-761-8712

Query Match 95.5%; Score 21; DB 9; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 227 TTCGAGTTCTCGATGAGAT 207

RESULT 7  
US-09-529-063-74/c  
Sequence 74, Application US/09529063  
Patent No. US20020102542A1  
GENERAL INFORMATION:  
APPLICANT: FUKUSHIMA, DAICHI  
APPLICANT: SHIBAYAMA, SHIRO  
APPLICANT: TADA, HIDEAKI

```

; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
; FILE REFERENCE: 058769
; CURRENT APPLICATION NUMBER: US/09/529,063
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/JP98/04514
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: JP 9-274674
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-529-063-74

Query Match          95.5%; Score 21; DB 9; Length 2061;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21
DB 186 TTCGAGTCTCGATGAGAT 166

RESULT 8
US-10-414-378-74/c
; Sequence 74, Application US/10414378
; Publication No. US20030165981A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, DAIKICHI
; APPLICANT: SHIBAYAMA, SHIRO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
; FILE REFERENCE: 058769
; CURRENT APPLICATION NUMBER: US/10/414,378
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/09/529,063
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/JP98/04514
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: JP 9-274674
; PRIOR FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-414-378-74

Query Match          95.5%; Score 21; DB 15; Length 2061;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21
DB 186 TTCGAGTCTCGATGAGAT 166

RESULT 9
US-10-011-370-1/c
; Sequence 1, Application US/10011370
; Publication No. US20020151704A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Kyaw, Hla
; APPLICANT: Pathirana, Marie Sudam
; APPLICANT: Smith, Kelli E.
; TITLE OF INVENTION: DNA Encoding Orphan SNORF10 Receptor
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; FILE REFERENCE: 58988
; CURRENT APPLICATION NUMBER: US/10/011,370
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US/09/286,085
; PRIOR FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 2231
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-011-370-1

Query Match          95.5%; Score 21; DB 13; Length 2231;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21
DB 258 TTCGAGTCTCGATGAGAT 238

RESULT 10
US-10-073-054-5/c
; Sequence 5, Application US/10073054
; Publication No. US20030167485A1
; GENERAL INFORMATION:
; APPLICANT: Garvan Institute of Medical Research
; APPLICANT: HERZOG, Herbert
; TITLE OF INVENTION: No. US20030167485A1 G-protein coupled receptor-encoding gene
; FILE REFERENCE: 1871-132 (93702-CIP/MRO)
; CURRENT APPLICATION NUMBER: US/10/073,054
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/308,596
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00805
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: AU P09386
; PRIOR FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human GPR56-3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (159)..(2237)
; OTHER INFORMATION:
; US-10-073-054-5

Query Match          95.5%; Score 21; DB 15; Length 2816;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTCTCGATGAGAT 21
DB 344 TTCGAGTCTCGATGAGAT 324

RESULT 11
US-10-295-027-767/c
; Sequence 767, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
```





RESULT 15  
US-10-460-479-1/c  
; Sequence 1, Application US/10460479  
; Publication No. US2004093627A1  
; GENERAL INFORMATION:  
; APPLICANT: Brennard, John Charles  
; APPLICANT: Hart, Kevin Anthony  
; TITLE OF INVENTION: Methods GPR56  
; FILE REFERENCE: 1991-220  
; CURRENT APPLICATION NUMBER: US/10/460,479  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: 09/845,771  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,422  
; PRIOR FILING DATE: 2000-05-03  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 1  
; LENGTH: 2822  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-460-479-1

Query Match 95.5%; Score 21; DB 16; Length 2822;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCTCGATGAGAT 21  
Db 348 TTCCGAGTTCTCGATGAGAT 328

RESULT 16  
US-10-322-281-337/c  
; Sequence 337, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 337  
; LENGTH: 2824  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-322-281-337

Query Match 95.5%; Score 21; DB 17; Length 2824;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCTCGATGAGAT 21  
Db 352 TTCCGAGTTCTCGATGAGAT 332

RESULT 17  
US-10-322-281-339/c  
; Sequence 339, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 339  
; LENGTH: 2824  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-322-281-339

Query Match 95.5%; Score 21; DB 17; Length 2824;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCTCGATGAGAT 21  
Db 352 TTCCGAGTTCTCGATGAGAT 332

RESULT 18  
US-09-529-063-75/c  
; Sequence 75, Application US/09529063  
; Patent No. US20020102542A1  
; GENERAL INFORMATION:  
; APPLICANT: FUKUSHIMA, DAIKICHI  
; APPLICANT: SHIBAYAMA, SHIRO  
; APPLICANT: TADA, HIDEAKI  
; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF  
; FILE REFERENCE: 058769  
; CURRENT APPLICATION NUMBER: US/09/529,063  
; CURRENT FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: PCT/JP98/04514  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: JP 9-274674  
; PRIOR FILING DATE: 1997-10-07  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 75  
; LENGTH: 3564  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: sig peptide  
; LOCATION: (43)..(2103)  
; NAME/KEY: mat peptide  
; LOCATION: (118)..(2103)  
; NAME/KEY: CDS  
; LOCATION: (43)..(2103)  
US-09-529-063-75

Query Match 95.5%; Score 21; DB 9; Length 3564;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGAGTTCTCGATGAGAT 21  
Db 228 TTCCGAGTTCTCGATGAGAT 208

RESULT 19  
US-10-414-378-75/c  
; Sequence 75, Application US/10414378  
; Publication No. US20030165981A1  
; GENERAL INFORMATION:  
; APPLICANT: FUKUSHIMA, DAIKICHI  
; APPLICANT: SHIBAYAMA, SHIRO  
; APPLICANT: TADA, HIDEAKI  
; TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF  
; FILE REFERENCE: 058769  
; CURRENT APPLICATION NUMBER: US/10/414,378  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: US/09/529,063  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: PCT/JP98/04514

PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: JP 9-274674  
PRIOR FILING DATE: 1997-10-07  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 75  
LENGTH: 3564  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: sig peptide  
LOCATION: (43)..(2103)  
FEATURE:  
NAME/KEY: mat peptide  
LOCATION: (118)..(2103)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (43)..(2103)  
US-10-414-378-75

Query Match 95.5%; Score 21; DB 15; Length 3564;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 228 TTCGAGTTCTCGATGAGAT 208

RESULT 20  
US-10-263-230A-8/C  
Sequence 8, Application US/10263230A  
Publication No. US20030152963A1  
GENERAL INFORMATION:  
APPLICANT: Duhl, David  
TITLE OF INVENTION: HUMAN CHROMOSOME 15 AND 16 BARDET-BIEDL  
FILE REFERENCE: 59516-243/PP-1568.002  
CURRENT FILING DATE: 2002-10-02  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 3686  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-263-230A-8

Query Match 95.5%; Score 21; DB 15; Length 3686;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 318 TTCGAGTTCTCGATGAGAT 298

RESULT 21  
US-10-073-054-3/C  
Sequence 3, Application US/10073054  
Publication No. US20030167485A1  
GENERAL INFORMATION:  
APPLICANT: Gargan Institute of Medical Research  
APPLICANT: HERZOG, Herbert  
TITLE OF INVENTION: NO. US20030167485A1 G-protein coupled receptor-encoding gene an  
FILE REFERENCE: 1871-132 (93702-CIP/MRO)  
CURRENT FILING DATE: 2002-02-12  
NUMBER OF SEQ ID NOS: 09/308,696  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00805

PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: AU P09386  
PRIOR FILING DATE: 1997-09-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 3  
LENGTH: 3711  
TYPE: DNA  
ORGANISM: human GPR56-2  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (168)..(2246)  
OTHER INFORMATION:  
US-10-073-054-3

Query Match 95.5%; Score 21; DB 15; Length 3711;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 353 TTCGAGTTCTCGATGAGAT 333

RESULT 22  
US-10-328-544-1/C  
Sequence 1, Application US/10328544  
Publication No. US20030175209A1  
GENERAL INFORMATION:  
APPLICANT: MUELLER, SABINE  
APPLICANT: GONZALEZ-ZULIETA, MIRELLA  
APPLICANT: FOHRER, ERIK  
APPLICANT: CHIN, DANIEL J.  
TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION  
FILE REFERENCE: AGT-008051  
CURRENT FILING DATE: 2002-12-23  
PRIOR APPLICATION NUMBER: US/10/328,544  
PRIOR FILING DATE: 2001-12-27  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 1  
LENGTH: 3711  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (168)..(2249)  
OTHER INFORMATION:  
US-10-328-544-1

Query Match 95.5%; Score 21; DB 15; Length 3711;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 353 TTCGAGTTCTCGATGAGAT 333

RESULT 23  
US-10-322-281-335/C  
Sequence 335, Application US/10322281  
Publication No. US20040126762A1  
GENERAL INFORMATION:  
APPLICANT: David W. Morris  
APPLICANT: Marc S. Malandino  
TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
FILE REFERENCE: 529452001000  
CURRENT FILING DATE: 2002-12-17  
NUMBER OF SEQ ID NOS: 866  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 335  
LENGTH: 3789  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-322-281-335

Query Match 95.5%; Score 21; DB 17; Length 3789;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
Db 333 TTCGAGTTCGATGAGAT 313

RESULT 24  
US-09-978-295A-482/c  
Sequence 482, Application US/09978295A  
Patent No. US2002015606A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kijavini, Ivay J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085523  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 9; Length 3819;

Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGTCTCGATGAGAT 21  
DB 399 TTGGAGTCTCGATGAGAT 379  
RESULT 25  
US-09-978-697-482/c  
Sequence 482, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deanoysers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078939  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079656  
 PRIOR FILING DATE: 1998-03-26  
 PRIOR APPLICATION NUMBER: 60/079664  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079689  
 PRIOR FILING DATE: 1998-03-27  
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 PRIOR FILING DATE: 1998-03-27  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5% Score 21; DB 9; Length 3819;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21.  
 DB 399 TTGGAGTTCTCGATGAGAT 379

RESULT 26  
US-09-978-192A-482/C  
Sequence 482, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Denoyere, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottfredsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-03  
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Query Match 95.5%; Score 21; DB 9; Length 3819;  
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTCTCGATGAGAT 21  
Db 399 TTCGAGTCTCGATGAGAT 379

RESULT 27  
US-09-999-832A-482/c  
; Sequence 482, Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferreira, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlson, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 9; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGAGTTCGATGAGAT 21  
Db 399 TTGGAGTTCGATGAGAT 379

RESULT 28  
US-09-978-189-482/c  
Sequence 482, Application US/09978189  
Publication No. US20030004102a1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Kijavlin, Ivar J.  
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APPLICANT: Napier, Mary A.  
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APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: 'us/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR FILING DATE: 1998-04-29

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTGGAGTTCTCGATGGAGAT 21
DB      399 TTGGAGTTCTCGATGGAGAT 379

RESULT 29
US-09-978-608A-482/c
; Sequence 482, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 482
; LENGTH: 3819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-482

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      399 TTGGAGTTCTCGATGGAGAT 379

RESULT 30
US-09-978-585A-482/c
; Sequence 482, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm

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SEQ ID NO 482  
LENGTH: 3819  
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ORGANISM: Homo sapiens  
US-09-978-585A-482

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 399 TTGGAGTTCTCGATGGAGAT 379

RESULT 31  
US-09-978-191A-482/C  
Sequence 482, Application US/09978191A  
Publication No. US2003050239A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnuyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavyn, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: US/09/978, 191A  
CURRENT FILING DATE: 2001-10-15  
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PRIOR APPLICATION NUMBER: 60/085697  
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Best Local Similarity 100.0%; Pred. No. 2.1;  
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Db 399 TTGGAGTTTCGATGAGAT 379  
RESULT 32  
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Sequence 482; Application US/09978403A  
Publication No. US20030050240A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deonoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
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PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
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PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336

PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-13  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21.  
DB 399 TTGGAGTTCTCGATGAGAT 379

RESULT 33  
US-09-978-564A-482/C  
Sequence 482, Application US/09978564A  
Publication No. US20030050241A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C25  
CURRENT APPLICATION NUMBER: US/09/978-564A  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/074450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664

PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
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PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR APPLICATION NUMBER: 60/081838  
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PRIOR APPLICATION NUMBER: 60/082568  
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PRIOR FILING DATE: 1998-04-22  
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PRIOR APPLICATION NUMBER: 60/082796  
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PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
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PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21  
DB 399 TTCGAGTTCGATGAGAT 379

RESULT 34  
US-09-999-833A-482/C  
Sequence 482, Application US/09999833A  
Publication No. US20030054405A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Denoyers, Luc  
APPLICANT: Baton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvarolf, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, U. Christopher  
APPLICANT: Gurney, Austen L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavrin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C65  
CURRENT APPLICATION NUMBER: US/09/999,833A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-03-30  
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PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
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PRIOR APPLICATION NUMBER: 60/081955  
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PRIOR APPLICATION NUMBER: 60/081838  
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PRIOR APPLICATION NUMBER: 60/082569  
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PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
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PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
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PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
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PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554

PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/08463  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCGATGAGAT 21  
DB 399 TTCGAGTTCGATGAGAT 379

RESULT 35  
US-09-981-915A-482/c  
Sequence 482, Application US/09981915A  
Publication No. US20030054986A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
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PRIOR FILING DATE: 1998-03-11  
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PRIOR APPLICATION NUMBER: 60/079728  
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PRIOR FILING DATE: 1998-03-30  
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PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105

PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-04-29

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PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
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PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity: 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCGATGAGAT 21  
DB 399 TTCCGAGTTCGATGAGAT 379

RESULT 36  
US-09-978-824-482/c  
Sequence 482, Application US/09978824  
Publication No. US20030055216A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C14  
CURRENT APPLICATION NUMBER: US/09/978,824  
PRIOR FILING DATE: 2001-10-17  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31



PRIOR APPLICATION NUMBER: 60/080327  
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PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441

PRIOR FILING DATE: 1998-05-06  
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTTCGATGAGAT 21  
DB 399 TTCCGAGTTTCGATGAGAT 379

RESULT 37  
US-09-918-585A-482/c  
Sequence 482, Application US/09918585A  
Publication No. US2003060406A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Fialavoff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C1  
CURRENT APPLICATION NUMBER: US/09/918,585A  
CURRENT FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
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PRIOR APPLICATION NUMBER: 60/083495  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR APPLICATION NUMBER: 60/084441  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-07

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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086023

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGAGTCTCGATGAGAT 21  
Db 399 TTGGAGTCTCGATGAGAT 379

RESULT 38  
US-09-999-834A-482/c  
Sequence 482, Application US/09999834A  
Publication No. US20030064407A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2630P1C75  
CURRENT APPLICATION NUMBER: US/09/999,834A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCGAGTTCGATGAGAT 21  
DB 399 TTCGAGTTCGATGAGAT 379

RESULT 39  
US-09-978-423A-482/c  
Sequence 482, Application US/09978423A  
Publication No. US2003069178A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Boccardo, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Pong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2650P1C21  
CURRENT APPLICATION NUMBER: US/09/978,423A  
CURRENT FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17

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63	PRIOR APPLICATION NUMBER: 60/081195
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65	PRIOR APPLICATION NUMBER: 60/081203
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67	PRIOR APPLICATION NUMBER: 60/081229
68	PRIOR FILING DATE: 1998-04-09
69	PRIOR APPLICATION NUMBER: 60/081955

PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081817
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PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29
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PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083466	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084411	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084634	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13

PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGTTCGATCGAGAT 21  
Db 399 TTCCGAGTTCGATCGAGAT 379

RESULT 40  
US-09-978-193A-482/c  
Sequence 482: Application US/0978193A  
Publication No. US20030073624A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Fliviaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC6  
CURRENT APPLICATION NUMBER: US/09/978,193A  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
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PRIOR FILING DATE: 1998-05-13  
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PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 399 TTGGAGTTCTCGATGAGAT 379  
RESULT 41  
US-09-99-830A-482/c  
Sequence 482, Application US/09999830A  
Publication No. US2003007700A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Batton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvarole, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Hillman, Austin L.  
APPLICANT: Hillman, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C70  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US/09/999,830A  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11



PRIOR APPLICATION NUMBER: 60/085697  
Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGAGTTCTCGATGAGAT 21  
DB 399 TTCGAGTTCTCGATGAGAT 379

RESULT 42  
US-09-978-757A-482/c

Sequence 482, Application US/09978757A  
Publication No. US20030083248A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC26  
CURRENT APPLICATION NUMBER: US/09/978,757A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
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PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936

PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-04-01  
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PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
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PRIOR APPLICATION NUMBER: 60/081229  
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PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
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PRIOR APPLICATION NUMBER: 60/082796  
 PRIOR FILING DATE: 1998-04-23  
 PRIOR APPLICATION NUMBER: 60/083336  
 PRIOR FILING DATE: 1998-04-27  
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 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/083392  
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 PRIOR FILING DATE: 1998-04-29  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTCGAGTTCGATGAGAT 21

DB 399 TTCGAGTTCGATGAGAT 379  
 RESULT 43  
 US-09-978-187B-482/c  
 Sequence 482, Application US/0978187B  
 Publication No. US20030096744A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deenoyers, Luc  
 APPLICANT: Batton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Geo, Wei-Qiang  
 APPLICANT: Geider, Hanspeter  
 APPLICANT: Gerritsen, Mary B.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P1C5  
 CURRENT FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
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 PRIOR FILING DATE: 1998-03-20  
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 PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
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PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392

PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR APPLICATION NUMBER: 60/084366  
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PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCGATGAGAT 21  
|||||  
Db 399 TTCGAGTTCGATGAGAT 379

RESULT 44  
US-09-978-643A-482/c  
; Sequence 482, Application US/09978643A

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/ Publication No. US20030104998A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Goddard, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C16
/ CURRENT APPLICATION NUMBER: US/09/978,643A
/ PRIORITY FILING DATE: 2001-10-16
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 482
/ LENGTH: 3819
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-978-643A-482

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCGATGAGAT 21
Db 399 TTCCGAGTTCGATGAGAT 379

RESULT 45
US-09-978-375A-482/C
/ Sequence 482, Application US/09978375A
/ Publication No. US20030130181A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Goddard, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavah, Ivar J.
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/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C24
/ CURRENT APPLICATION NUMBER: US/09/978,375A
/ PRIORITY FILING DATE: 2002-04-19
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 482
/ LENGTH: 3819
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-978-375A-482

Query Match          95.5%; Score 21; DB 10; Length 3819;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTTCGATGAGAT 21
Db 399 TTCCGAGTTCGATGAGAT 379

RESULT 46
US-09-978-298A-482/C
/ Sequence 482, Application US/09978298A
/ Publication No. US20030134785A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Goddard, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavah, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C2
/ CURRENT APPLICATION NUMBER: US/09/978,298A
/ PRIORITY FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
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2	PRIOR FILING DATE: 1997-11-03
3	PRIOR APPLICATION NUMBER: 60/065111
4	PRIOR FILING DATE: 1997-11-13
5	PRIOR APPLICATION NUMBER: 60/06364
6	PRIOR FILING DATE: 1997-11-21
7	PRIOR APPLICATION NUMBER: 60/077450
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9	PRIOR APPLICATION NUMBER: 60/077632
10	PRIOR FILING DATE: 1998-03-11
11	PRIOR APPLICATION NUMBER: 60/077641
12	PRIOR FILING DATE: 1998-03-11
13	PRIOR APPLICATION NUMBER: 60/077649
14	PRIOR FILING DATE: 1998-03-11
15	PRIOR APPLICATION NUMBER: 60/077791
16	PRIOR FILING DATE: 1998-03-12
17	PRIOR APPLICATION NUMBER: 60/078004
18	PRIOR FILING DATE: 1998-03-13
19	PRIOR APPLICATION NUMBER: 60/078886
20	PRIOR FILING DATE: 1998-03-20
21	PRIOR APPLICATION NUMBER: 60/078936
22	PRIOR FILING DATE: 1998-03-20
23	PRIOR APPLICATION NUMBER: 60/078910
24	PRIOR FILING DATE: 1998-03-20
25	PRIOR APPLICATION NUMBER: 60/078939
26	PRIOR FILING DATE: 1998-03-20
27	PRIOR APPLICATION NUMBER: 60/079294
28	PRIOR FILING DATE: 1998-03-25
29	PRIOR APPLICATION NUMBER: 60/079656
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31	PRIOR APPLICATION NUMBER: 60/079664
32	PRIOR FILING DATE: 1998-03-27
33	PRIOR APPLICATION NUMBER: 60/079689
34	PRIOR FILING DATE: 1998-03-27
35	PRIOR APPLICATION NUMBER: 60/079663
36	PRIOR FILING DATE: 1998-03-27
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43	PRIOR APPLICATION NUMBER: 60/079923
44	PRIOR FILING DATE: 1998-03-30
45	PRIOR APPLICATION NUMBER: 60/080105
46	PRIOR FILING DATE: 1998-03-31
47	PRIOR APPLICATION NUMBER: 60/080107
48	PRIOR FILING DATE: 1998-03-31
49	PRIOR APPLICATION NUMBER: 60/080155
50	PRIOR FILING DATE: 1998-03-31
51	PRIOR APPLICATION NUMBER: 60/080194
52	PRIOR FILING DATE: 1998-03-31
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54	PRIOR FILING DATE: 1998-04-01
55	PRIOR APPLICATION NUMBER: 60/080328
56	PRIOR FILING DATE: 1998-04-01
57	PRIOR APPLICATION NUMBER: 60/080333
58	PRIOR FILING DATE: 1998-04-01
59	PRIOR APPLICATION NUMBER: 60/080344
60	PRIOR FILING DATE: 1998-04-01
61	PRIOR APPLICATION NUMBER: 60/081195
62	PRIOR FILING DATE: 1998-04-08
63	PRIOR APPLICATION NUMBER: 60/081203
64	PRIOR FILING DATE: 1998-04-09
65	PRIOR APPLICATION NUMBER: 60/081228
66	PRIOR FILING DATE: 1998-04-09
67	PRIOR APPLICATION NUMBER: 60/081955

PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081819
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081952
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PRIOR APPLICATION NUMBER:	60/082568
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PRIOR APPLICATION NUMBER:	60/082700
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PRIOR APPLICATION NUMBER:	60/082797
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PRIOR APPLICATION NUMBER:	60/082796
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PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085333
PRIOR FILING DATE:	1998-05-13

PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGAGTCTCGATGAGAT 21  
Db 399 TTCCGAGTCTCGATGAGAT 379

RESULT 47  
US-09-978-188A-482/C  
Sequence 482, Application US/09978188A  
Publication No. US20030139328A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Baton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P263091C8  
CURRENT APPLICATION NUMBER: US/09/978,188A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-03-10  
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PRIOR FILING DATE: 1998-05-13  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGTTCTCGATGAGAT 21  
DB 399 TTGGAGTTCTCGATGAGAT 379

RESULT 48  
US-09-978-681A-482/c  
Sequence 482, Application US/09978681A  
Publication No. US20030195148A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C18  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: US/09/978, 681A  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11



PRIOR APPLICATION NUMBER: 60/085697

Query Match 95.5%; Score 21; DB 10; Length 3819;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGAGTTCTCGATGAGAT 21  
Db 399 TTCGAGTTCTCGATGAGAT 379

RESULT 49  
US-09-978-194A-482/c  
Sequence 482, Application US/09978194A  
Publication No. US2003019533A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C10  
CURRENT APPLICATION NUMBER: US/09/978, 194A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
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PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
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PRIOR APPLICATION NUMBER: 60/078936

PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
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PRIOR APPLICATION NUMBER: 60/079656  
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Db 399 TTCGAGTTCGATGAGAT 379

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Publication No. US20030195344A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C1  
CURRENT APPLICATION NUMBER: US/09/999, 829A  
CURRENT FILING DATE: 2002-03-19  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 482  
LENGTH: 3819  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-999-829A-482

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Search completed: February 2, 2005, 01:34:12  
Job time : 450 secs.